

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:11:24 ; Search time 16 Seconds
(without alignments)
1052.371 Million cell updates/sec

Title: 10032108-2EDIT
Perfect score: 901
Sequence: 1 MTPLGPASSLPOSFLRLCLE.....SHLQSFLEVSRYVLRHLAQP 175
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	887	98.4	204	1 FQHUGL	granulocyte colony
2	875.5	97.2	207	2 A24573	granulocyte colony
3	741	82.2	194	2 T09255	granulocyte colony
4	735	81.6	174	2 T10268	granulocyte colony
5	636	70.6	208	2 A26496	granulocyte colony
6	629	69.8	214	2 JC5043	granulocyte colony
7	301	33.4	201	2 A42247	myelomonocytic gro
8	103.5	11.5	212	2 I46590	interleukin 6 - pi
9	103.5	11.5	212	2 I46521	prointerleukin 6
10	95	10.5	208	2 T09216	interleukin-6 prec
11	94	10.4	345	2 C82270	hypothetical prote
12	89	9.9	502	2 A46506	H+-transporting tw
13	88.5	9.8	666	2 A87577	oligopeptide trans
14	86.5	9.6	2175	1 S03170	homeotic protein c
15	85.5	9.5	786	2 F83292	probable sensor/re
16	84	9.3	208	1 A56610	interleukin-6 prec
17	83.5	9.3	207	2 I46084	interleukin 6 - ca
18	81	9.0	274	1 C69362	conserved hypothet
19	80.5	8.9	406	2 B72766	probable threonyl-
20	80.5	8.9	846	2 JC7721	aryl hydrocarbon r
21	80	8.9	474	2 D75550	probable D-alanyl-
22	79.5	8.8	316	2 H82958	homoserine kinase
23	79.5	8.8	325	2 T41921	hypothetical prote
24	79	8.8	423	2 AC3553	4-aminobutyrate tr
25	79	8.8	469	2 AD1926	hypothetical prote
26	77.5	8.6	254	2 S37424	probable oxidoredu
27	77.5	8.6	506	2 T07942	probable squalene
28	77.5	8.6	653	2 C82580	oligopeptide trans
29	76.5	8.5	195	2 JH0680	ciliary neurotroph

ALIGNMENTS

RESULT 1

FOHUGL

granulocyte colony-stimulating factor precursor - human

N;Alternate names: colony-stimulating factor 3; G-CSF

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1988 #sequence revision 18-Aug-1995 #text_change 09-Jul-2004

C;Accession: A25093; A49796; A47587; S68331

R;Nagata, S.; Tsuchiya, M.; Asano, S.; Yamamoto, O.; Hirata, Y.; Kubota, N.; Oheda, M.;

EMBO J. 5, 575-581, 1986

A;Title: The chromosomal gene structure and two mRNAs for human granulocyte colony-stimul

A;Reference number: A25093; MUID:86220137; PMID:2423327

A;Accession: A25093

A;Molecule type: DNA: mRNA

A;Residues: 1-204 <NAG>

A;Cross-references: UNIPROT:P09919; EMBL:X03656; EMBL:X03655; NID:g31693; PIDN:CAA27290.1

R;Devlin, J.J.; Devlin, P.E.; Myambo, K.; Lilly, M.B.; Rado, T.A.; Warren, M.K.

J. Leukoc. Biol. 41, 302-306, 1987

A;Title: Expression of granulocyte colony-stimulating factor by human cell lines.

A;Reference number: A49796; MUID:87196936; PMID:3494801

A;Accession: A49796

A;Molecule type: mRNA

A;Residues: 1-204 <DEV>

A;Cross-references: GB:M17706; NID:g183040; PIDN:AAA35882.1; PID:g183041

R;Souza, L.M.; Boons, T.C.; Gabrilove, J.; Lai, P.H.; Zeebo, K.M.; Murdock, D.C.; Chazin,

Science 232, 61-65, 1986

A;Title: Recombinant human granulocyte colony-stimulating factor: effects on normal and

A;Reference number: A47587; MUID:86151684; PMID:2420009

A;Accession: A47587

A;Molecule type: mRNA

A;Residues: 19-204 <SOU>

A;Cross-references: GB:M13008; NID:g183044; PIDN:AAA03056.1; PID:g183045

R;Hantu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.

Arch. Biochem. Biophys. 324, 344-356, 1995

A;Title: Extracellular domain of granulocyte-colony stimulating factor receptor.

A;Reference number: S68331; MUID:96132662; PMID:8554326

A;Accession: S68331

A;Molecule type: protein

A;Residues: 'W',31-46 <HAN>

C;Genetics:

A;Gene: GDB:CSF3

A;Cross-references: GDB:119083; OMIM:138970

A;Map position: 17q11.2-17q12

A;Introns: 14/1, 65/3, 101/3, 150/3

C;Function:

A;Description: stimulates the differentiation and proliferation of hematopoietic progenit

C;Superfamily: Interleukin-6

C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer

F;1-30/Domain: signal sequence #status predicted <SIG>

F;31-204/Product: granulocyte colony-stimulating factor #status predicted <MAT>

F;66-72,94-104/Disulfide bonds: #status predicted

R;Tsuchiya, M.; Kaziro, Y.; Nagata, S.
Eur. J. Biochem. 165, 7-12, 1987
A;Title: The chromosomal gene structure for murine granulocyte colony-stimulating factor
A;Reference number: A29536; MUID:87190474; PMID:3494605
A;Accession: A29536
A;Molecule type: DNA
A;Residues: 1-208 <TSU>
A;Cross-references: UNIPROT:P09920; GB:X05402; NID:G51059; PIDN:CAA28986.1; PID:G51060
R;Tsuchiya, M.; Asano, S.; Kaziro, Y.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 83, 7633-7637, 1986
A;Title: Isolation and characterization of the cDNA for murine granulocyte colony-stimulating factor
A;Reference number: A26496; MUID:87017003; PMID:3489940
A;Accession: A26496
A;Molecule type: mRNA
A;Residues: 1-208 <FS2>
A;Cross-references: UNIPROT:P13926; NID:G193451; PIDN:AAA37672.1; PID:G309248
R;Simpson, R.J.; Nice, E.C.; Nicola, N.A.
Biol. Chem. Hoppe-Seyler 368, 1327-1331, 1987
A;Title: Structural studies on the murine granulocyte colony-stimulating factor.
A;Reference number: S02493; MUID:88106998; PMID:3501294
A;Accession: S02493
A;Status: preliminary
A;Molecule type: protein
A;Residues: 31-34, 'X', 36-43; 48-51, 'X', 53-57, 'X', 60-71; 159-164, 'X', 166-176; 183-198, 'X', 200-208
C;Genetics: 14/1; 71/3; 107/3; 156/3
A;Introns: 14/1; 71/3; 107/3; 156/3
C;Superfamily: interleukin-6
C;Keywords: cytokine; growth factor; macrophage; monomer

Query Match 70.6%; Score 636; DB 2; Length 208;
Best Local Similarity 73.4%; Pred. No. 3.6e-53;
Matches 127; Conservative 13; Mismatches 33; Indels 0; Gaps 0;

QY 1 MTPGLPASSLPQSFLLRCLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 36 VSLPPLPSLPFRSLKSLSEQVRKIQASGVLEQLCATYKLCPELVLLGHSIGIPKA 95
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADPATTIWO 120
DB 96 SLSCSSQALQOQTKCLSQLHSGFLYQGLLQALSGISPALPTLDLQDVANFATTIWO 155
QY 121 QMEELGMAPALQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLA 173
DB 156 QMENLGVAFTVQTSAMPFTAFORRAGGVLAISYLOGLFLETARLHLA 208

RESULT 6
JCS043
granulocyte colony-stimulating factor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: JCS043
R;Han, S.W.; Ramesh, N.; Osborne, W.R.A.
Gene 175, 101-104, 1996
A;Title: Cloning and expression of the cDNA encoding rat granulocyte colony-stimulating factor
A;Reference number: JCS043; MUID:97074656; PMID:8917083
A;Accession: JCS043
A;Molecule type: mRNA
A;Residues: 1-214 <HAN>
A;Cross-references: UNIPROT:P97712; GB:U37101; NID:G1680658; PIDN:AACS2915.1; PID:G16806
A;Experimental source: skin fibroblasts
C;Comment: This receptor acts on precursor hemopoietic cells to control the production of interleukin-6
C;Superfamily: interleukin-6
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-214/Product: granulocyte colony-stimulating factor #status predicted <MAT>

Query Match 69.8%; Score 629; DB 2; Length 214;
Best Local Similarity 71.4%; Pred. No. 1.7e-52;
Matches 125; Conservative 14; Mismatches 36; Indels 0; Gaps 0;

QY 1 MTPGLPASSLPQSFLLRCLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 27 VSSLPPLPSLPFRSLKSLSEQVRKIQARNTLEQLCATYKLCPELVLLGHSIGIPKA 86

QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADPATTIWO 120
DB 87 SLSCSSQALQOQTKCLSQLHSGFLYQGLLQALSGISPALPTLDLQDVANFATTIWO 146
QY 121 QMEELGMAPALQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 147 QMESLGVAFTVQTSMTFTSFARAGGVLTSTYLOSLFLETARLHLPRP 201

RESULT 7
A42247
myelomonocytic growth factor precursor - chicken
N;Alternate names: colony-stimulating factor CMGF
C;Species: Gallus gallus (chicken)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42247; S03633
R;Sterneck, E.; Blattner, C.; Graf, T.; Leutz, A.
Mol. Cell. Biol. 12, 1728-1735, 1992
A;Title: Structure of the chicken myelomonocytic growth factor gene and specific activation of the gene
A;Reference number: A42247; MUID:92195319; PMID:1549124
A;Accession: A42247
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-201 <STE>
A;Cross-references: UNIPROT:P13854
A;Note: sequence extracted from NCBI backbone (NCBIN:89832, NCBIP:89836)
R;Leutz, A.; Damm, K.; Sterneck, E.; Kowenz, E.; Frank, R.; Gausepohl, H.; Pan, E.M.O. J. 8, 175-181, 1989
A;Title: Molecular cloning of the chicken myelomonocytic growth factor (CMGF) reveals relationship to interleukin-6
A;Reference number: S03633; MUID:89231616; PMID:2785450
A;Accession: S03633
A;Molecule type: mRNA
A;Residues: 1-201 <LEU>
A;Cross-references: EMBL:X14477; NID:G63596; PIDN:CAA32639.1; PID:G63597
C;Superfamily: interleukin-6
C;Keywords: glycoprotein

Query Match 33.4%; Score 301; DB 2; Length 201;
Best Local Similarity 40.0%; Pred. No. 2.7e-21;
Matches 66; Conservative 29; Mismatches 68; Indels 2; Gaps 1;

QY 12 QSFLLRCLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWAPLSSCPQALQ 71
DB 36 QLFHLKXLEFTKIRGDVAALQAVCDTFLCTEELQLVQDPHVLQAPLDOCHKRGFQ 95
QY 72 LAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADPATTIWOQMEELGMAPAL 131
DB 96 AEVCFQIRAGLHAYHDSLGAVLRLLPNHTTLVETLQDLAANLSSNIQQOMEDGLDVT 155
QY 132 QPTQ--GAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQ 174
DB 156 LPAEQRSPPTFTSGPPQQVGGFFILANQRFLETAYRALRLAR 200

RESULT 8
I46590
interleukin 6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46590
R;Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A;Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation conceptuses
A;Reference number: I46590; MUID:92360284; PMID:1497880
A;Accession: I46590
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <MAT>
A;Cross-references: UNIPROT:P26893; GB:M80258; NID:G164514; PIDN:AAC27127.1; PID:G164515

A;Accession: S03170
A;Molecule type: mRNA
A;Residues: 1-2175 <BLO>
C;Cross-references: UNIPROT:P10180; EMBL:X07985; NID:g7767; PIDN:CAG30794.1; PID:g7768

C;Genetics:
A;Gene: cut
A;Cross-references: FlyBase:FBgn0004198
C;Superfamily: homeotic protein cut; cut repeat homology; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;886-958/DNA domain: cut repeat homology <CU1>
F;1339-1411/DNA domain: cut repeat homology <CU2>
F;1617-1689/DNA domain: cut repeat homology <CU3>
F;1746-1802/DNA domain: homeobox homology <HOX>

Query Match 9.6%; Score 86.5; DB 1; Length 2175;
Best Local Similarity 23.1%; Pred. No. 13;
Matches 34; Conservative 21; Mismatches 61; Indels 31; Gaps 3;

Qy 28 DGAAQLERLCATYRLCHPEELVLLGSLGLPWPALSSCPAQALACLSQLHSGFLFY Q 87
Db 1404 DENAVHKLVASQYKIA-PEKLMTGTYSGPSMP-----Q 1437

Qy 88 GLLALEGISPELGPTLTDLTDVDADFATTIWOOMEELGMWAPALOPTQGAMPAFASA FOR 147
Db 1438 GLASKMQRAASPWKMSSELKLPQAQHLMQMOMAMSAAMQQOQ-----VAQAQQQ 1492

Qy 148 RAGGVLVASHLQSFLVSRYRVLRLHAQ 174
Db 1493 AQAQAQAHLQQAQAQAHLQQAQAHLQQA 1519

RESULT 15
F83292
probable sensor/response regulator hybrid PA2824 [imported] - Pseudomonas aeruginosa (str)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83292
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
. J.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: AB2950; PMID:20437337; PMID:10984043
A;Accession: F83292
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-786 <STO>
A;Cross-references: UNIPROT:Q91019; GB:AEO04709; GB:AEO04091; NID:g9948904; PIDN:AAG0621
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2824

Query Match 9.5%; Score 85.5; DB 2; Length 786;
Best Local Similarity 28.7%; Pred. No. 4.6;
Matches 49; Conservative 20; Mismatches 49; Indels 53; Gaps 10;

Qy 27 GDGAALQRCLCATYRLCHPBELVLLG--HSIGIPWPLSCPSQAIQLAG-CILSQLHQSG 82
Db 490 GLGLALTAKUCEANMGELTVETVGSLFSVGLPLVPSP-PLOALPLGRVIAQC SAN 548

Qy 83 LFYLQGLLQALEGISPE-----LGPTLDTLQDADVADFTTIWOOMEELGMA 128
Db 549 -----SGLAQLIQTWLRPMGLEVKRLTDDSLGHSLDVLI SDPCDCU-----MGLR 595

Qy 129 PALOPTQGA MP AFASAFOR AGGV LV AS HQ SF L --EVSYRV--LRHLAQP 175
Db 596 PSI-----GTPILLVTAYGSFLFEPLARRSPLQLARP 629

Search completed: December 27, 2004, 13:12:09
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:11:24 ; Search time 63.5 Seconds
(without alignments)
1585.678 Million cell updates/sec

Title: 10032108-2EDIT
Perfect score: 901
Sequence: 1 WPLGFPASLPQSLFLRLCLE.....SHLQSFLEVSIVRLRLAQP 175

-Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	887	98.4	200	2	Q8N4W3
2	875.5	97.2	207	1	CSF3 HUMAN
3	741	82.2	194	1	CSF3 FELCA
4	741	82.2	195	2	Q9GJU0
5	736	81.7	175	1	CSF3 CANFA
6	735	81.6	174	1	CSF3 SHEEP
7	724	80.4	195	1	CSF3 BOVIN
8	699	77.6	195	1	CSF3 PIG
9	636	70.6	208	1	CSF3 MOUSE
10	629	69.8	214	2	P97712
11	511	56.7	127	2	Q8MKE0
12	301	33.4	201	1	MGF_CHICK
13	109	12.1	241	2	Q90Y10
14	107.5	11.9	212	2	Q8MJ75
15	106	11.8	208	2	Q9XT80
16	103.5	11.5	212	1	IL6 PIG
17	99	11.0	205	1	IL6_ORCOR
18	95	10.5	208	1	IL6_HORSE
19	94.5	10.5	455	2	Q8D706
20	94	10.4	345	2	Q9KTL6
21	92	10.2	189	2	Q6N282
22	92	10.2	189	2	Q9H2A5
23	92	10.2	189	2	Ah66267
24	91	10.1	208	1	IL6 FELCA
25	90.5	10.0	1931	2	Q8RJY3
26	89	9.9	189	2	Q9NPF7
27	89	9.9	189	2	Ah66268
28	89	9.9	189	2	AAQ89442
29	89	9.9	189	2	Ah67511
30	89	9.9	189	2	AAH67512
31	89	9.9	189	2	AAH67513

32	89	9.9	502	2	Q34008
33	89	9.9	788	2	Q8CF87
34	89	9.9	850	2	Q7TQ21
35	89	9.9	851	2	Q8CF88
36	89	9.9	852	2	Q811T9
37	88.5	9.8	666	2	Q9A523
38	87	9.7	189	2	Q6NZ80
39	87	9.7	189	2	Ah66269
40	87	9.7	290	2	Q9POS7
41	86.5	9.6	214	2	Q8MKES
42	86.5	9.6	2175	1	HMCU DROME
43	85.5	9.5	503	2	Q6D3M5
44	85.5	9.5	786	2	Q9I019
45	85	9.4	193	2	Q9N2H9

ALIGNMENTS

RESULT 1

Q8N4W3	PRELIMINARY;	PRT;	200 AA.
AC Q8N4W3;			
DT 01-OCT-2002 (Tremblrel. 22, Created)			
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)			
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE Colony stimulating factor 3, isoform c.			
GN Name=CSF3;			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Skin;			
RX MEDLINE=22388957; PubMed=12477932;			
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,			
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.			
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,			
RA Jones S.J., Marra M.A.			
RT "Generation and initial analysis of more than 15,000 full-length human			
RT and mouse cDNA sequences.";			
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN [2]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Skin;			
RA Strausberg R.L.			
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
RL EMBL; BC033245; AAH33245.1; -			
DR HSSP; P09919; 1GNC.			
DR GO; GO:0005576; C:extracellular; IEA.			
DR GO; GO:0005125; F:cytokine activity; IEA.			
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.			
DR GO; GO:0006955; P:immune response; IEA.			
DR InterPro; IPR009079; 4 helix cytokine.			
DR InterPro; IPR003629; GCSF MGF.			
DR InterPro; IPR003573; IL6_MGF_GCSF.			
DR InterPro; IPR003574; Interleukin_6.			
DR Pfam; PF00489; IL6; 1.			
DR PRINTS; PR00433; IL6GCSFMGF.			


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DR EMBL: AF388025; AAK62469.1; -.
DR EMBL: M17706; AAA35882.1; -.
DR PIR: A24573; A24573.
DR PIR: A25093; FQHUGL.
DR PDB: 1CD9; X-ray; A/C=30-207.
DR PDB: 1GNC; NMR; @=30-207.
DR PDB: 1PGR; X-ray; A/C/E/G=30-207.
DR PDB: 1RHG; X-ray; A/B/C=31-207.
DR Genew; HGNC:2438; CSF3.
DR MIM; 138970; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005130; F:granulocyte colony-stimulating factor recep. . .; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW 3D-structure: Alternative splicing; Cytokine; Glycoprotein;
KW Growth factor; Pharmaceutical; Polymorphism; Signal.
FT SIGNAL 1 30 Granulocyte colony-stimulating factor.
FT CHAIN 31 207
FT DISULFID 69 75
FT DISULFID 97 107
FT CARBOHYD 166 166
FT VARSPIC 66 68
FT VARIANT 157 157 L -> M (in dbSNP:2227329).
FT VARIANT 174 174 A -> T (in dbSNP:2227330).
FT HELIX 41 65
FT HELIX 69 71
FT HELIX 77 86
FT TURN 87 88
FT HELIX 105 124
FT TURN 125 127
FT TURN 130 132
FT TURN 133 156
FT TURN 157 158
FT HELIX 176 203
FT TURN 204 204
SQ SEQUENCE 207 AA; 22293 MW; 421F635ECCT776996 CRC64;
Query Match 97.2%; Score 875.5; DB 1; Length 207;
Best Local Similarity 96.6%; Pred. No. 2.5e-71;
Matches 171; Conservative 3; Mismatches 0; Indels 3; Gaps 1;
QY 2 TPLGPASSLPQSFLRLCLQVVKIQGDGAALQERL---CATYELCHPELVLLGHSLGIP 58
DB 31 TPLGPASSLPQSFLRLCLQVVKIQGDGAALQERLSECATYKLCHEPELVLLGHSLGIP 90
QY 59 WAPLSSCPQALQACLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTI 118
DB 91 WAPLSSCPQALQACLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTI 150
QY 119 WQMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVRLHQAQ 175
DB 151 WQMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVRLHQAQ 207
RESULT 3
ID CSF3_FELCA STANDARD; PRT; 194 AA.
AC 002708;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF) (Fragment).
GN Name=CSF3;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=European shorthair; TISSUE=Lung;
RA MEDLINE=21389237; PubMed=11497496; DOI=10.1006/cyto.2001.0910;
RX Dunham S.P., Onions D.E.;
RT "Isolation, nucleotide sequence and expression of a cDNA encoding
RL feline granulocyte colony-stimulating factor.";
CC Cytokine 14:347-351(2001).
CC -!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: O-glycosylated (By similarity).
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Y08558; CAA69853.1; -.
CC PIR: T09255; T09255.
CC HSP; P09919; 1RHG.
CC InterPro; IPR009079; 4 helix cytokine.
CC InterPro; IPR003629; GCSF_MGF.
CC InterPro; IPR003573; IL6_MGF_GCSF.
CC InterPro; IPR003574; Interleukin_6.
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC ProDom; PD008388; GCSF_MGF; 1.
CC SMART; SM00126; IL6; 1.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT NON_TER 1
FT SIGNAL <1 20 Potential.
FT CHAIN 21 194 Granulocyte colony-stimulating factor.
FT DISULFID 56 62 By similarity.
FT DISULFID 84 94 By similarity.
FT CARBOHYD 153 153 O-linked (GalNAc...) (By similarity).
FT SEQUENCE 194 AA; 21154 MW; F72B7AB3DAE7385E CRC64;
Query Match 82.2%; Score 741; DB 1; Length 194;
Best Local Similarity 80.5%; Pred. No. 3.8e-59;
Matches 140; Conservative 12; Mismatches 22; Indels 0; Gaps 0;
QY 2 TPLGPASSLPQSFLRLCLQVVKIQGDGAALQERLCAVRLCHPELVLLGHSLGIPWAP 61
DB 21 TPLGPTSSLPQSFLKCLQVVKVQADGALQERLCAHKLCHPELVLLGHSLGIPQAP 80
QY 62 LSSCPSQALQALQACLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTI 121
DB 81 LSSCPSQALQALQACLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTI 140
QY 122 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVRLHQAQ 175
DB 141 MEDVGNAPAVPPTQGTMTFTTSAFORRAGGTLVASNLQSFLEVSRYVRLHFTKP 194
RESULT 4
Q9GUUO PRELIMINARY; PRT; 195 AA.
ID Q9GUUO
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Q9GUU0;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Granulocyte colony-stimulating factor precursor.
GN Name-G-CSF;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
[1]
RN MEDLINE=2151548; PubMed=11675019;
RX Yamamoto A., Iwata A., Tsuchiya K., Katsumata A., Oishi K., Saito T.,
RA Tsujimoto H., Hasegawa A., Ueda S.;
RT "Molecular cloning and expression of the cDNA encoding feline
granulocyte colony-stimulating factor.";
RL Gene 274:263-269 (2001).
DR EMBL; AB042552; BAB17789.1; -.
DR EMBL; AB042553; BAB17757.1; -.
DR HSP; P09919; IAHG.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW SIGNAL.
FT SIGNAL 1 22 Potential.
SQ SEQUENCE 195 AA; 21255 MW; 544C682909412FCF CRC64;
Query Match 82.2%; Score 741; DB 2; Length 195;
Best Local Similarity 80.5%; Pred. No. 3.8e-59;
Matches 140; Conservative 12; Mismatches 22; Indels 0; Gaps 0;
Qy 2 TPLGPASSLPOSFLRLCQLQVRIQGGAAALQERLCATYRLCHPEELVLLGHSIGIPWAP 61
Db 22 TPLGTPSSLPQSLFLKCLQVRIQGGAAALQERLCATYRLCHPEELVLLGHSIGIPWAP 81
Qy 62 LSSCPQALQAGCLSQLHSLGLFLYQGLLQALAGISPELGTLDLTLDVADFAATTIQQ 121
Db 82 LSSCSQALQAGCLSQLHSLGLFLYQGLLQALAGISPELGTLDLTLDVADFAATTIQQ 141
Qy 122 MEELGMALOPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYRLHLAQP 175
Db 142 MEDVGMAPVPTQGTMTFTTSAPORRAGGVVASHLQSFLEVSRYRLHLAQP 195
RESULT 5
CSF3_CANFA STANDARD; PRT; 175 AA.
AC P35834;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte colony-stimulating factor (G-CSF).
GN Name-CSF3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RX MEDLINE=94076341; PubMed=7504736;
RA Lovejoy B., Cascio D., Eisenberg J.;
"Crystal structure of canine and bovine granulocyte-colony stimulating factor (G-CSF).";
J. Mol. Biol. 234:640-653 (1993).
-!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages. This CSF induces granulocytes.
-!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-6 superfamily.
PDB; 1BGD; X-ray; @=1-175.
PDB; 1BGE; X-ray; A/B=1-175.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003629; GCSF_MGF.
InterPro; IPR003573; IL6_MGF_GCSF.
Pfam; PF00489; IL6; 1.
PRINTS; PR00433; IL6GCSFMGF.
ProDom; PD008388; GCSF_MGF; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
3D-structure; Cytokine; Glycoprotein; Growth factor.
DISULFID 37 43
DISULFID 65 75
FT CARBOHYD 134 134 O-linked (GalNAc...) (By similarity).
FT STRAND 10 10
FT HELIX 12 39
FT HELIX 45 55
FT TURN 56 56
FT TURN 63 65
FT TURN 67 69
FT TURN 72 92
FT TURN 93 95
FT TURN 98 100
FT HELIX 101 125
FT TURN 126 126
FT HELIX 144 171
FT TURN 172 172
FT STRAND 173 173
SQ SEQUENCE 175 AA; 18858 MW; 28C26B24990C6DB3 CRC64;
Query Match 81.7%; Score 736; DB 1; Length 175;
Best Local Similarity 80.0%; Pred. No. 9.6e-59;
Matches 140; Conservative 12; Mismatches 23; Indels 0; Gaps 0;
Qy 1 MPLGPASSLPOSFLRLCQLQVRIQGGAAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
Db 1 MAPLGTGFLPQSLFLKCLQVRIQGGAAALQERLCATYRLCHPEELVLLGHSIGIPQ 60
Qy 61 PLSSCPQALQAGCLSQLHSLGLFLYQGLLQALAGISPELGTLDLTLDVADFAATTIQQ 120
Db 61 PLSSCSQALQAGCLSQLHSLGLFLYQGLLQALAGISPELGTLDLTLDVADFAATTIQQ 120
Qy 121 QMEELGMALOPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYRLHLAQP 175
Db 121 QMEDLGMAPVPTQGTMTFTTSAPORRAGGVVASHLQSFLEVSRYRLHLAQP 175
RESULT 6
CSF3_SHEEP STANDARD; PRT; 174 AA.
AC Q28746;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor (G-CSF).
GN Name-CSF3;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;

RP SEQUENCE FROM N.A.
RX MEDLINE=95102116; PubMed=7528579;
RA O'Brien P.M., Seow H.P., Rothel J.S., Wood P.R.;
RT "Cloning and sequencing of an ovine granulocyte colony-stimulating
RT factor cDNA";
RL DNA Seq. 4:339-342(1994).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L07939; AAA68006.1; -.
DR PIR; T10268; T10268.
DR HSSP; P09919; IRHG.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor.
FT DISULFID 36 42 By similarity.
FT DISULFID 64 74 By similarity.
FT CARBOHYD 133 133 O-linked (GalNAc...) (By similarity).
SQ SEQUENCE 174 AA; 18806 MW; BA5AA8F8D23ACD1E CRC64;

Query Match 81.6%; Score 735; DB 1; Length 174;
Best Local Similarity 81.6%; Pred. No. 1.2e-58;
Matches 142; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 2 TPLGPASSLPQSFLRLCQVRKIQDGAALQERLCATYRLCHPELVLLHSLGIPWAP 61
DB 1 TPLGPARSUPQSFLRLCQVRKIQDGAALQERLCATYRLCHPELVLLHSLGIPQAP 60

QY 62 LSSCPSQALQAGCLSQLHSGFLYQGLLQALAGISPELGPTLDTLQLDVADPATTIWOQ 121
DB 61 LSSCPSQSLSLTCLDQLHGLFLYQGLLQALAGISPELAPTLDLTLDVADPATTIWLQ 120

QY 122 MEELGWAPALQPTQAMPAPASAFQRRAGVLVASHLQSFLEVSVYRLHLAQP 175
DB 121 MEDLGVAQVPTQGTMTPTSAFQRRAGVLVASHLQSFLEVSVYRLHLAEP 174

RESULT 7
CSF3_BOVIN STANDARD; PRT; 195 AA.
ID CSF3_BOVIN
AC P35833; Q9TV89;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN Names=CSF3; Synonyms=GCSF;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;

RP SEQUENCE FROM N.A.
RC STRAIN=Holstein;
RA Heidari M., Kehrl M.E. Jr.;
RT "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte
RT colony stimulating factor";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=94076341; PubMed=7504736;
RA Lovejoy B., Cascio D., Eisenberg D.;
RT "Crystal structure of canine and bovine granulocyte-colony stimulating
RT factor (G-CSF)";
RL J. Mol. Biol. 234:640-653(1993).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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CC
CC EMBL; AF092533; AAD16102.1; -.
DR PDB; 1BGC; X-ray; @=22-195.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW 3D-structure; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 195 Granulocyte colony-stimulating factor.
FT DISULFID 57 63
FT DISULFID 85 95
FT CARBOHYD 134 134
FT CONFLICT 93 94
FT HELIX 32 60
FT HELIX 65 69
FT TURN 70 71
FT TURN 72 75
FT TURN 76 76
FT HELIX 83 85
FT TURN 87 89
FT HELIX 92 112
FT TURN 113 115
FT TURN 118 120
FT HELIX 121 145
FT HELIX 164 191
FT TURN 192 192
SQ SEQUENCE 195 AA; 21431 MW; 8C06119E4ADFBA73 CRC64;

Query Match 80.4%; Score 724; DB 1; Length 195;
Best Local Similarity 80.5%; Pred. No. 1.3e-57;
Matches 140; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 2 TPLGPASSLPQSFLRLCQVRKIQDGAALQERLCATYRLCHPELVLLHSLGIPWAP 61
DB 22 TPLGPARSUPQSFLRLCQVRKIQDGAALQERLCATYRLCHPELVLLHSLGIPQAP 81

QY 62 LSSCPSQALQAGCLSQLHSGFLYQGLLQALAGISPELGPTLDTLQLDVADPATTIWOQ 121

Db 82 LSSCSQSLSLQNLHGGVLYQGLLQALAGISPELAPLDTLQDVTDFATNIWLQ 141
 QY 122 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSLFVSVTVRLHQAOP 175
 Db 142 MEDLGAAPVQPTQGAMPPTFTSAFORRAGGVLVASQLHRFLELAVRGLYLAEP 195

RESULT 8

CSF3_PIG STANDARD; PRT; 195 AA.
 AC 002837; 019180;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF).
 GN Names=CSF3;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9623;
 [1]
 RP SEQUENCE FROM N.A.
 RA Kulmburg P.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Gloster S.E., Sandeman R.M., Strom A.D.G.;
 RT "Cloning of a cDNA and gene encoding porcine granulocyte-colony
 stimulating factor.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 cytokines that act in hematopoiesis by controlling the production,
 differentiation, and function of 2 related white cell populations
 of the blood, the granulocytes and the monocytes-macrophages. This
 CSF induces granulocytes (By similarity).
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: O-glycosylated (By similarity).
 CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
 CC
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 CC
 CC EMBL; Y10494; CAA71518.1; -
 CC EMBL; U68482; AAB70701.1; -
 CC EMBL; U68481; AAB70700.1; -
 CC HSSP; P09919; IRRG.
 CC InterPro; IPR009079; 4_helix_cytokine.
 CC InterPro; IPR003629; GCSF_MGF.
 CC InterPro; IPR003573; IL6_MGF_GCSF.
 CC Pfam; PF00489; IL6; 1
 CC PRINTS; PR00433; IL6GCSFMGF.
 CC ProDom; PD008388; GCSF_MGF; 1.
 CC SMART; SM00126; IL6; 1.
 CC PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 195
 FT DISULFID 57 63
 FT DISULFID 85 95
 FT CARBOHYD 154 154
 FT CONFLICT 123 123 A -> R (in Ref. 1).
 SQ SEQUENCE 195 AA; 21214 MW; 84787E20B0BAEALC CRC64;
 Query Match 77.6%; Score 699; DB 1; Length 195;
 Best Local Similarity 78.6%; Pred. No. 2.5e-55;

Matches 136; Conservative 12; Mismatches 25; Indels 0; Gaps 0;
 QY 3 PLGPASSLPQSFLRCLQEVQRKIQDGAALQERLCATYRLCHPELVLLGHSLGIPWAPL 62
 Db 23 PLSPASSLPQSFLRCLQEVQRKIQDGAALQERLCATYRLCHPELVLLGHSLGIPWAPL 82
 QY 63 SSCPSQALQALAGCSLSHLSGLFLYQGLLQALAGISPELAPLDTLQDVTDFATNIWQ 122
 Db 83 SSCSSQALQALAGCSLSHLSGLFLYQGLLQALAGISPELAPLDTLQDVTDFATNIWQ 142
 QY 123 EELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSLFVSVTVRLHQAOP 175
 Db 143 EDLRNAPASLPTQGTVPFTFTSAFORRAGGVLVASHLQSLFVSVTVRLHQAOP 195

RESULT 9

CSF3_MOUSE STANDARD; PRT; 208 AA.
 AC P09920;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF).
 GN Name=CSf3; Synonyms=Csfg;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=87017003; PubMed=3489940;
 RX Tsuchiya M., Asano S., Kaziro Y., Nagata S.;
 RA "Isolation and characterization of the cDNA for murine granulocyte
 colony-stimulating factor.";
 RT Proc. Natl. Acad. Sci. U.S.A. 83:7633-7637(1986).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=87190474; PubMed=3494605;
 RX Tsuchiya M., Kaziro Y., Nagata S.;
 RA "The chromosomal gene structure for murine granulocyte colony-
 stimulating factor.";
 RT Eur. J. Biochem. 165:7-12(1987).
 RL [3]
 RP PARTIAL SEQUENCE.
 RX PubMed=3501294;
 RA Simpson R.J., Nice E.C., Nicola N.A.;
 RT "Structural studies on the murine granulocyte colony-stimulating
 factor.";
 RL Biol. Chem. Hoppe-Seyler 368:1327-1331(1987).
 CC -!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 cytokines that act in hematopoiesis by controlling the production,
 differentiation, and function of 2 related white cell populations
 of the blood, the granulocytes and the monocytes-macrophages. This
 CSF induces granulocytes.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: O-glycosylated (By similarity).
 CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
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 CC
 CC EMBL; M13926; AAA37672.1; -
 CC EMBL; X05402; CAA38986.1; -
 CC PIR; A29536; A26496.
 CC HSSP; P09919; IRRG.
 CC MGI; MGI:1339751; Csfg.
 CC InterPro; IPR009079; 4_helix_cytokine.
 CC

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9231616; PubMed=2785450;
 RA Leutz A., Damm K., Sterneck E., Kowenz E., Ness S., Frank R.,
 RA Gausepohl H., Pan Y.-C.E., Smart J., Hayman M., Graf T.;
 RT "Molecular cloning of the chicken myelomonocytic growth factor (CMGF)
 RT reveals relationship to interleukin 6 and granulocyte colony
 RT stimulating factor";
 RL EMBO J. 8:175-181(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92195319; PubMed=1549124;
 RA Sterneck E., Blattner C., Graf T., Leutz A.;
 RT "Structure of the chicken myelomonocytic growth factor gene and
 RT specific activation of its promoter in avian myelomonocytic cells by
 RT protein kinases";
 RL Mol. Cell. Biol. 12:1728-1735(1992).
 CC -!- FUNCTION: Hematopoietic growth factor that stimulates the
 CC proliferation and colony formation of normal and transformed avian
 CC cells of the myeloid lineage.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M85034; AAA48694.1; -;
 DR EMBL; X14477; CAA32639.1; -;
 DR F1R; A42247; A42247.
 DR HSSP; P09919; 1RHG.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003629; GCSP MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD008388; GCSP MGF; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 201 Myelomonocytic growth factor.
 FT DISULFID 61 67 By similarity.
 FT DISULFID 89 99 By similarity.
 FT CARBOHYD 123 123 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 137 137 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 201 AA; 22373 MW; 240A8DD21B4244E6 CRC64;
 Query Match 33.4%; Score 301; DB 1; Length 201;
 Best Local Similarity 40.0%; Pred. No. 3.3e-19;
 Matches 66; Conservative 29; Mismatches 68; Indels 2; Gaps 1;
 QY 12 QSFLLCLQVRKIQDGAALQRLCATYRLCHPEELVLIGHSLGIPWAPLSSCPQALQ 71
 Db 36 QLFHKNLEFTRKIRGVAALQRAVCDTQCLCTEELQLVQPPHVLVQAPLQDCKRGQ 95
 QY 72 LAGCLQLHSLGLPYOGLQALREGISPELPTDITLDQVADPATTIWOQMEELGNAPAL 131
 Db 96 AEVCFQIRAGLHAYHDSGLAVLRLLPNHTTLVETLQLDAANLSNIQQQMEDLGLDVT 155
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 ID Q90Y10
 AC Q90Y10;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Interleukin-6 precursor.
 GN Name=IL-6;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RA Kaiser P., Rothwell L., Galyov E.E., Barrow P.A., Burnside J.,
 RA Wigley P.;
 RT "Differential cytokine expression in avian cells in response to
 RT invasion by Salmonella typhimurium, Salmonella enteritidis and
 RT Salmonella gallinarum";
 RL Microbiology 146:3217-3226(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kaiser P.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ309540; CAC40812.1; -;
 DR EMBL; AJ250838; CAC15566.2; -;
 DR HSSP; P05231; 1ALU.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003629; GCSP MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD008388; GCSP MGF; 1.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
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 FT SIGNAL 1 47 Potential.
 FT CHAIN 48 241 mature CHIL-6.
 SQ SEQUENCE 241 AA; 26790 MW; 657F8049F25BD2F8 CRC64;
 Query Match 12.1%; Score 109; DB 2; Length 241;
 Best Local Similarity 22.2%; Pred. No. 0.11;
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 QY 45 PEELVLGHSLGIPWAPLSSCPQALQALAG-----CLSHSLGLFLYQGLQALREGISPE 99
 Db 101 NSMEMLVRNNINLP----KVTEEDCLLAGFPDEECLTKLSGLFAFQYLFQIETPDS 156
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 Db 157 EKQNVESLCYSTKHLAATIRQV-----INPDEVWIP--DSAAQKSLLANLKSQDW 206
 QY 154 ---VASHL-----QSFLVSRYVLRHL 172
 Db 207 IEKITHLILRDTFTSFMEKTVRAVRYL 233

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:14:34 ; Search time 297.5 Seconds
(without alignments)
211.245 Million cell updates/sec

Title: 10032108-2EDIT
Perfect score: 901
Sequence: 1 MTPGLPASSLPQSLRLCLE.....SHLQSFLEVSRYRLRLAQP 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTU5_PUBCOMB.pep.*
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 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	901	100.0	175	9	US-09-754-532-72
2	901	100.0	175	14	US-10-032-108-72
3	898	99.7	175	9	US-09-754-532-74
4	898	99.7	175	14	US-10-032-108-74
5	895	99.3	175	9	US-09-754-532-67
6	895	99.3	175	9	US-09-754-532-69
7	895	99.3	175	9	US-09-754-532-70
8	895	99.3	175	9	US-09-754-532-71
9	895	99.3	175	9	US-09-754-532-73
10	895	99.3	175	9	US-09-754-532-75
11	895	99.3	175	14	US-10-032-108-67
12	895	99.3	175	14	US-10-032-108-69
13	895	99.3	175	14	US-10-032-108-70
14	895	99.3	175	9	US-09-754-532-72
15	895	99.3	175	14	US-10-032-108-72
16	895	99.3	175	9	US-09-754-532-74
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19	895	99.3	175	9	US-09-754-532-69
20	895	99.3	175	9	US-09-754-532-70
21	895	99.3	175	9	US-09-754-532-71
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14	895	99.3	175	14	US-10-032-108-71	Sequence 71, Appl
15	895	99.3	175	14	US-10-032-108-73	Sequence 73, Appl
16	895	99.3	175	14	US-10-032-108-75	Sequence 75, Appl
17	892	99.0	175	9	US-09-754-532-2	Sequence 2, Appl
18	892	99.0	175	9	US-09-230-733-1	Sequence 1, Appl
19	892	99.0	175	9	US-09-921-114-2	Sequence 2, Appl
20	892	99.0	175	11	US-09-817-725-2	Sequence 2, Appl
21	892	99.0	175	14	US-10-131-956-2	Sequence 2, Appl
22	892	99.0	175	14	US-10-264-846-2	Sequence 2, Appl
23	892	99.0	175	14	US-10-009-792A-21	Sequence 21, Appl
24	892	99.0	175	14	US-10-032-108-2	Sequence 2, Appl
25	892	99.0	175	14	US-10-345-639A-2	Sequence 2, Appl
26	892	99.0	175	14	US-10-365-418-1	Sequence 1, Appl
27	892	99.0	175	14	US-10-436-784-2	Sequence 2, Appl
28	892	99.0	175	14	US-10-168-956A-3	Sequence 3, Appl
29	892	99.0	175	15	US-10-632-695-15	Sequence 15, Appl
30	892	99.0	175	16	US-10-659-295-38	Sequence 38, Appl
31	892	99.0	175	16	US-10-750-797-2	Sequence 2, Appl
32	892	99.0	175	17	US-10-751-242-2	Sequence 2, Appl
33	889	98.7	175	9	US-09-754-532-68	Sequence 68, Appl
34	889	98.7	175	9	US-09-754-532-76	Sequence 76, Appl
35	889	98.7	175	9	US-09-754-532-83	Sequence 83, Appl
36	889	98.7	175	9	US-09-754-532-92	Sequence 92, Appl
37	889	98.7	175	9	US-09-754-532-93	Sequence 93, Appl
38	889	98.7	175	9	US-09-754-532-99	Sequence 99, Appl
39	889	98.7	175	9	US-09-754-532-100	Sequence 100, Appl
40	889	98.7	175	9	US-09-818-430A-2	Sequence 2, Appl
41	889	98.7	175	14	US-10-032-108-68	Sequence 68, Appl
42	889	98.7	175	14	US-10-032-108-76	Sequence 76, Appl
43	889	98.7	175	14	US-10-032-108-83	Sequence 83, Appl
44	889	98.7	175	14	US-10-032-108-92	Sequence 92, Appl
45	889	98.7	175	14	US-10-032-108-93	Sequence 93, Appl

ALIGNMENTS

RESULT 1
US-09-754-532-72
; Sequence 72, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-72

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Best Local Similarity 100.0%; Pred. No. 7.8e-83;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-032-108-72
; Sequence 72, Application US/10032108
; Publication No. US20030171559A1
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; FILE REFERENCE: 01017/38834F
; CURRENT APPLICATION NUMBER: US/10/032,108
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/754,532
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: US 09/304,186
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 09/027,508
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/956,812
; PRIOR FILING DATE: 1987-10-23
; PRIOR APPLICATION NUMBER: US 08/448,716
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: US 08/010,099
; PRIOR FILING DATE: 1993-01-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent-In ver. 3.1
; SEQ ID NO 72
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: G-CSF analog
US-10-032-108-72

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Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-754-532-74

; Sequence 74, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-74

Query Match 99.7%; Score 898; DB 9; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.6e-82;
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RESULT 4
US-10-032-108-74
; Sequence 74, Application US/10032108
; Publication No. US20030171559A1
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; FILE REFERENCE: 01017/38834F
; CURRENT APPLICATION NUMBER: US/10/032,108
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/754,532
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: US 09/304,186
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 09/027,508
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/956,812

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; PRIOR FILING DATE: 1987-10-23
; PRIOR APPLICATION NUMBER: US 08/448,716
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: US 08/010,099
; PRIOR FILING DATE: 1993-01-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent-In ver. 3.1
; SEQ ID NO 74
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: G-CSF analog
US-10-032-108-74

Query Match          99.7%; Score 898; DB 14; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.6e-82;
Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPBEVLVLLGHSIGIPWA 60
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RESULT 5
US-09-754-532-67
; Sequence 67, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-67

Query Match          99.7%; Score 898; DB 14; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.6e-82;
Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPBEVLVLLGHSIGIPWA 60
DB 1 MTPGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPBEVLVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADFATTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADFATTIWQ 120
QY 121 QMEELGMALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSYRVLRLHQAOP 175
DB 121 QMEELGMALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSYRVLRLHQAOP 175

RESULT 5
US-09-754-532-67
; Sequence 67, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-67

Query Match          99.3%; Score 895; DB 9; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPBEVLVLLGHSIGIPWA 60
DB 1 MTPGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPBEVLVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADFATTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADFATTIWQ 120
QY 121 QMEELGMALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSYRVLRLHQAOP 175
DB 121 QMEELGMALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSYRVLRLHQAOP 175

Query Match          99.3%; Score 895; DB 9; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPBEVLVLLGHSIGIPWA 60
DB 1 MTPGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPBEVLVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADFATTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLQDVADFATTIWQ 120
QY 121 QMEELGMALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSYRVLRLHQAOP 175
DB 121 QMEELGMALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSYRVLRLHQAOP 175
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```
RESULT 7
US-09-754-532-70
; Sequence 70, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: Angen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-70

Query Match          99.3%; Score 895; DB 9; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTPLGPASSLPQSFLRLCQLKQVRIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
Db      1 MTPLGPASSLPQSFLRLCQLKQVRIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60

QY      61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTDLQDVADFTATIQ 120
Db      61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTDLQDVADFTATIQ 120

QY      121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175
Db      121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175

RESULT 8
US-09-754-532-71
; Sequence 71, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: Angen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
```

```
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-71

Query Match          99.3%; Score 895; DB 9; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTPLGPASSLPQSFLRLCQLKQVRIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
Db      1 MTPLGPASSLPQSFLRLCQLKQVRIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60

QY      61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTDLQDVADFTATIQ 120
Db      61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTDLQDVADFTATIQ 120

QY      121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175
Db      121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175

RESULT 9
US-09-754-532-73
; Sequence 73, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: Angen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-73

Query Match      99.3%; Score 895; DB 9; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTDLTLDLQDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTDLTLDLQDVADFATTIQQ 120
QY 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 10
US-09-754-532-75
; Sequence 75, Application US/09754532
; Patent No. US2001001619A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-75

Query Match      99.3%; Score 895; DB 9; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
```

```
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTDLTLDLQDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTDLTLDLQDVADFATTIQQ 120
QY 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 11
US-10-032-108-67
; Sequence 67, Application US/10032108
; Publication No. US20030171559A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; FILE REFERENCE: 01017/38834F
; CURRENT APPLICATION NUMBER: US/10/032,108
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/754,532
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: US 09/304,186
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 09/027,508
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/956,812
; PRIOR FILING DATE: 1987-10-23
; PRIOR APPLICATION NUMBER: US 08/448,716
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: US 08/010,099
; PRIOR FILING DATE: 1993-01-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent-In ver. 3.1
; SEQ ID NO 67
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: G-CSF analog
US-10-032-108-67

Query Match      99.3%; Score 895; DB 14; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTDLTLDLQDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTDLTLDLQDVADFATTIQQ 120
QY 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 12
US-10-032-108-69
; Sequence 69, Application US/10032108
; Publication No. US20030171559A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; FILE REFERENCE: 01017/38834F
; CURRENT APPLICATION NUMBER: US/10/032,108
```

Query Match 99.3%; Score 895; DB 14; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 09/754,532
PRIOR FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: US 09/304,186
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 08/956,812
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 08/448,716
PRIOR FILING DATE: 1995-05-24
PRIOR APPLICATION NUMBER: US 08/010,099
PRIOR FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patent-In ver. 3.1
SEQ ID NO 69
LENGTH: 175
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: G-CSF analog
US-10-032-108-69

Query Match 99.3%; Score 895; DB 14; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 09/754,532
PRIOR FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: US 09/304,186
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 08/956,812
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 08/448,716
PRIOR FILING DATE: 1995-05-24
PRIOR APPLICATION NUMBER: US 08/010,099
PRIOR FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patent-In ver. 3.1
SEQ ID NO 70
LENGTH: 175
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: G-CSF analog
US-10-032-108-70

Query Match 99.3%; Score 895; DB 14; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 09/754,532
PRIOR FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: US 09/304,186
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 08/956,812
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 08/448,716
PRIOR FILING DATE: 1995-05-24
PRIOR APPLICATION NUMBER: US 08/010,099
PRIOR FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patent-In ver. 3.1
SEQ ID NO 71
LENGTH: 175
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: G-CSF analog
US-10-032-108-71

Query Match 99.3%; Score 895; DB 14; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 09/754,532
PRIOR FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: US 09/304,186
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 08/956,812
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 08/448,716
PRIOR FILING DATE: 1995-05-24
PRIOR APPLICATION NUMBER: US 08/010,099
PRIOR FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patent-In ver. 3.1
SEQ ID NO 69
LENGTH: 175
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: G-CSF analog
US-10-032-108-69

Query Match 99.3%; Score 895; DB 14; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 09/754,532
PRIOR FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: US 09/304,186
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 08/956,812
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 08/448,716
PRIOR FILING DATE: 1995-05-24
PRIOR APPLICATION NUMBER: US 08/010,099
PRIOR FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patent-In ver. 3.1
SEQ ID NO 71
LENGTH: 175
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: G-CSF analog
US-10-032-108-71

Query Match 99.3%; Score 895; DB 14; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 09/754,532
PRIOR FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: US 09/304,186
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 08/956,812
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 08/448,716
PRIOR FILING DATE: 1995-05-24
PRIOR APPLICATION NUMBER: US 08/010,099
PRIOR FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patent-In ver. 3.1
SEQ ID NO 70
LENGTH: 175
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: G-CSF analog
US-10-032-108-70

Query Match 99.3%; Score 895; DB 14; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 09/754,532
PRIOR FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: US 09/304,186
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 08/956,812
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 08/448,716
PRIOR FILING DATE: 1995-05-24
PRIOR APPLICATION NUMBER: US 08/010,099
PRIOR FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patent-In ver. 3.1
SEQ ID NO 71
LENGTH: 175
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: G-CSF analog
US-10-032-108-71

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; CURRENT APPLICATION NUMBER: US/10/032,108
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/754,532
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: US 09/304,186
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 09/027,508
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/956,812
; PRIOR FILING DATE: 1987-10-23
; PRIOR APPLICATION NUMBER: US 08/448,716
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: US 08/010,099
; PRIOR FILING DATE: 1993-01-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent-In ver. 3.1
; SEQ ID NO 73
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: G-CSF analog
US-10-032-108-73

Query Match      99.3%; Score 895; DB 14; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MTPFGPASSLPQSGFLRLCLQGVKIQGDGAALQERLCATYRLCHPELVLLGHSLGIPWA 60
Db      1  MTPFGPASSLPQSGFLRLCLQGVKIQGDGAALQERLCATYRLCHPELVLLGHSLGIPWA 60

Qy      61  PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTLDTLQLDVADEFATTIWQ 120
Db      61  PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTLDTLQLDVADEFATTIWQ 120

Qy      121  QMEELGNAPALQPTQGMPPAFAPAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 175
Db      121  QMEELGNAPALQPTQGMPPAFAPAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 175
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Search completed: December 27, 2004, 13:34:27
Job time : 297.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:11:24 ; Search time 20 Seconds
(without alignments)
580.283 Million cell updates/sec

Title: 10032108-2EDIT
Perfect score: 901
Sequence: 1 MTPPLGASSLPQSFLLRCLE.....SHLQSFLEVSRYRLRLAQP 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCITUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfilese1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	901	100.0	175	1 US-08-010-099-72	Sequence 72, Appl
2	901	100.0	175	1 US-08-448-716-72	Sequence 72, Appl
3	901	100.0	175	3 US-09-304-186-72	Sequence 72, Appl
4	901	100.0	175	4 US-09-754-532-72	Sequence 72, Appl
5	898	99.7	175	1 US-08-010-099-74	Sequence 74, Appl
6	898	99.7	175	1 US-08-448-716-74	Sequence 74, Appl
7	898	99.7	175	3 US-09-304-186-74	Sequence 74, Appl
8	898	99.7	175	4 US-09-754-532-74	Sequence 74, Appl
9	895	99.3	175	1 US-08-010-099-67	Sequence 67, Appl
10	895	99.3	175	1 US-08-010-099-69	Sequence 69, Appl
11	895	99.3	175	1 US-08-010-099-70	Sequence 70, Appl
12	895	99.3	175	1 US-08-010-099-71	Sequence 71, Appl
13	895	99.3	175	1 US-08-010-099-73	Sequence 73, Appl
14	895	99.3	175	1 US-08-010-099-75	Sequence 75, Appl
15	895	99.3	175	1 US-08-448-716-67	Sequence 67, Appl
16	895	99.3	175	1 US-08-448-716-69	Sequence 69, Appl
17	895	99.3	175	1 US-08-448-716-70	Sequence 70, Appl
18	895	99.3	175	1 US-08-448-716-71	Sequence 71, Appl
19	895	99.3	175	1 US-08-448-716-73	Sequence 73, Appl
20	895	99.3	175	1 US-08-448-716-75	Sequence 75, Appl
21	895	99.3	175	3 US-09-304-186-67	Sequence 67, Appl
22	895	99.3	175	3 US-09-304-186-69	Sequence 69, Appl
23	895	99.3	175	3 US-09-304-186-70	Sequence 70, Appl
24	895	99.3	175	3 US-09-304-186-71	Sequence 71, Appl
25	895	99.3	175	3 US-09-304-186-73	Sequence 73, Appl
26	895	99.3	175	3 US-09-304-186-75	Sequence 75, Appl
27	895	99.3	175	4 US-09-754-532-67	Sequence 67, Appl

28	895	99.3	175	4 US-09-754-532-69	Sequence 69, Appl
29	895	99.3	175	4 US-09-754-532-70	Sequence 70, Appl
30	895	99.3	175	4 US-09-754-532-71	Sequence 71, Appl
31	895	99.3	175	4 US-09-754-532-73	Sequence 73, Appl
32	895	99.3	175	4 US-09-754-532-75	Sequence 75, Appl
33	892	99.0	175	1 US-08-010-099-2	Sequence 2, Appl
34	892	99.0	175	1 US-08-167-721-1	Sequence 1, Appl
35	892	99.0	175	1 US-08-428-732-6	Sequence 6, Appl
36	892	99.0	175	1 US-08-448-716-2	Sequence 2, Appl
37	892	99.0	175	2 US-08-321-510-2	Sequence 2, Appl
38	892	99.0	175	2 US-08-879-760-2	Sequence 2, Appl
39	892	99.0	175	3 US-09-304-186-2	Sequence 2, Appl
40	892	99.0	175	4 US-09-230-733-1	Sequence 1, Appl
41	892	99.0	175	4 US-09-479-313B-15	Sequence 15, Appl
42	892	99.0	175	4 US-09-754-532-2	Sequence 2, Appl
43	892	99.0	175	5 PCT-US95-01729-2	Sequence 2, Appl
44	889	98.7	175	1 US-08-010-099-68	Sequence 68, Appl
45	889	98.7	175	1 US-08-010-099-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1
US-08-010-099-72
; Sequence 72, Application US/08010099
; Patent No. 5581476
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen, Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/010,099
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-010-099-72

Query Match 100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.7e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTPLGPASSLPQSFLLRCLEQVRKIQDGAALQERLCATYRLCHPPELVLLGSLGPWA	60
DB	1	MTPLGPASSLPQSFLLRCLEQVRKIQDGAALQERLCATYRLCHPPELVLLGSLGPWA	60
QY	61	PLSSCPQALQAGCISQLHSGFLYQGLQALEGISPELPTDLTQLQDVAFTTIWQ	120
DB	61	PLSSCPQALQAGCISQLHSGFLYQGLQALEGISPELPTDLTQLQDVAFTTIWQ	120

QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 175
Db 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 175

RESULT 2

US-08-448-716-72
; Sequence 72, Application US/08448716
; Patent No. 5790421
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,716
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-448-716-72

Query Match 100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.7e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCLQEQVKIQGDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
Db 1 MTPLGPASSLPQSFLRLCLQEQVKIQGDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
QY 61 PLSSCPSQLAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIWQ 120
Db 61 PLSSCPSQLAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIWQ 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 175
Db 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 175

RESULT 3

US-09-304-186-72
; Sequence 72, Application US/09304186
; Patent No. 6261550
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California

; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/304,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-304-186-72

Query Match 100.0%; Score 901; DB 3; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.7e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLRLCLQEQVKIQGDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
Db 1 MTPLGPASSLPQSFLRLCLQEQVKIQGDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
QY 61 PLSSCPSQLAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIWQ 120
Db 61 PLSSCPSQLAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIWQ 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 175
Db 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 175

RESULT 4

US-09-754-532-72
; Sequence 72, Application US/09754532
; Patent No. 6632426
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-5725
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-754-532-72

Query Match 100.0%; Score 901; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.7e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGASSLPQSFLRLCQLQVRRIOGDGAALQERLCATYRLCHPELVLLGHSGLGIPWA 60
DB 1 MTPLGASSLPQSFLRLCQLQVRRIOGDGAALQERLCATYRLCHPELVLLGHSGLGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSLGFLYQGLLQALEGISPELGPTDLTLDQDVADPATTIQ 120
DB 61 PLSSCPQALQAGCLSQLHSLGFLYQGLLQALEGISPELGPTDLTLDQDVADPATTIQ 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 5
US-08-010-099-74
Sequence 74, Application US/08010099
Patent No. 5581476
GENERAL INFORMATION:
APPLICANT: Osslund, Timothy D.
TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: Amgen Center, 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/010,099
FILING DATE: 24-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-5725
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-010-099-74

Query Match 99.7%; Score 898; DB 1; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.9e-91;
Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGASSLPQSFLRLCQLQVRRIOGDGAALQERLCATYRLCHPELVLLGHSGLGIPWA 60

DB 1 MTPLGASSLPQSFLRLCQLQVRRIOGDGAALQERLCATYRLCHPELVLLGHSGLGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSLGFLYQGLLQALEGISPELGPTDLTLDQDVADPATTIQ 120
DB 61 PLSSCPQALQAGCLSQLHSLGFLYQGLLQALEGISPELGPTDLTLDQDVADPATTIQ 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 6
US-08-448-716-74
Sequence 74, Application US/08448716
Patent No. 5790421
GENERAL INFORMATION:
APPLICANT: Osslund, Timothy D.
TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: Amgen Center, 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States of America
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,716
FILING DATE: 24-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-5725
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-448-716-74

Query Match 99.7%; Score 898; DB 1; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.9e-91;
Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGASSLPQSFLRLCQLQVRRIOGDGAALQERLCATYRLCHPELVLLGHSGLGIPWA 60
DB 1 MTPLGASSLPQSFLRLCQLQVRRIOGDGAALQERLCATYRLCHPELVLLGHSGLGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSLGFLYQGLLQALEGISPELGPTDLTLDQDVADPATTIQ 120
DB 61 PLSSCPQALQAGCLSQLHSLGFLYQGLLQALEGISPELGPTDLTLDQDVADPATTIQ 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 7
US-09-304-186-74
Sequence 74, Application US/09304186
Patent No. 6261550
GENERAL INFORMATION:
APPLICANT: Osslund, Timothy D.

;; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
;; NUMBER OF SEQUENCES: 110
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Amgen Inc.
;; STREET: Amgen Center, 1840 DeHavilland Drive
;; CITY: Thousand Oaks
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 91320-1789
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/304,186
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/448,716
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pessin, Karol
;; REGISTRATION NUMBER: 34,899
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 805/499-5725
;; TELEFAX: 805/499-8011
;; INFORMATION FOR SEQ ID NO: 74:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 175 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-304-186-74

Query Match 99.7%; Score 898; DB 3; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.9e-91;
Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLRLCLQVRRKIQDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLQVRRKIQDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
QY 61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDVADFAFTTIWQ 120
DB 61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDVADFAFTTIWQ 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 8
US-09-754-532-74
;; Sequence 74, Application US/09/54532
;; Patent No. 6632426
;; GENERAL INFORMATION:
;; APPLICANT: Oselund, Timothy D.
;; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
;; NUMBER OF SEQUENCES: 110
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Amgen Inc.
;; STREET: Amgen Center, 1840 DeHavilland Drive
;; CITY: Thousand Oaks
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 91320-1789
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/754,532
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/448,716
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pessin, Karol
;; REGISTRATION NUMBER: 34,899
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 805/499-5725
;; TELEFAX: 805/499-8011
;; INFORMATION FOR SEQ ID NO: 74:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 175 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-754-532-74

Query Match 99.7%; Score 898; DB 4; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.9e-91;
Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLRLCLQVRRKIQDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLQVRRKIQDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
QY 61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDVADFAFTTIWQ 120
DB 61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDVADFAFTTIWQ 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 9
US-08-010-099-67
;; Sequence 67, Application US/08010099
;; Patent No. 5581476
;; GENERAL INFORMATION:
;; APPLICANT: Oselund, Timothy
;; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
;; NUMBER OF SEQUENCES: 110
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Amgen, Inc.
;; STREET: Amgen Center, 1840 DeHavilland Drive
;; CITY: Thousand Oaks
;; STATE: California
;; COUNTRY: USA
;; ZIP: 91320-1789
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/010,099
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pessin, Karol
;; REGISTRATION NUMBER: 34,899
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 805/499-5725
;; TELEFAX: 805/499-8011
;; INFORMATION FOR SEQ ID NO: 67:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 175 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein


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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/010,099
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-8011
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-010-099-71

Query Match 99.3%; Score 895; DB 1; Length 175;
Best Local Similarity 98.9%; Pred. No. 4e-91;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCLQEVKIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLQEVKIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLVADVATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLVADVATTIQQ 120
QY 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 14
US-08-010-099-75
Sequence 75, Application US/08010099
Patent No. 5581476
GENERAL INFORMATION:
APPLICANT: Osslund, Timothy
TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: Amgen Center, 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/010,099
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-5725
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-010-099-75

Query Match 99.3%; Score 895; DB 1; Length 175;
Best Local Similarity 98.9%; Pred. No. 4e-91;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCLQEVKIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLQEVKIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLVADVATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDLVADVATTIQQ 120
QY 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/010,099
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-8011
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
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RESULT 15

US-08-448-716-67
; Sequence 67, Application US/08448716
; Patent No. 5790421
; GENERAL INFORMATION:
; APPLICANT: Oslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,716
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-448-716-67

Query Match 99.3%; Score 895; DB 1; Length 175;
Best Local Similarity 98.9%; Pred. No. 4e-91;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCQLQVVKIQGDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
|||
Db 1 MTPLGPASSLPQSFLRLCQLQVVKIQGDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
|||

QY 61 PLSSCPQSALQALAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLQDVADFATTIWQ 120
|||
Db 61 PLSSCPQSALQALAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLQDVADFATTIWQ 120
|||

QY 121 QMEELGMALOPTQGMAPAFASAFORRAGGVLVASHLOSFEVSVYRLRHQAQP 175
|||
Db 121 QMEELGMALOPTQGMAPAFASAFORRAGGVLVASHLOSFEVSVYRLRHQAQP 175
|||

Search completed: December 27, 2004, 13:17:22
Job time : 21 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:11:24 ; Search time 63.5 Seconds
(without alignments)
1585.678 Million cell updates/sec

Title: 10032108-2

Perfect score: 901

Sequence: 1 MTPGLPASSLPQSLFKLCLE.....SHLQSFLEVSRYVLRHLAQP 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374546 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	896	99.4	200	Q8N4W3	Q8N4W3 homo sapien
2	884.5	98.2	207	1 CSF3 HUMAN	P09919 homo sapien
3	744	82.6	194	1 CSF3 FELCA	O02708 felis silve
4	744	82.6	195	2 Q9GJU0	O9GJU0 felis silve
5	739	82.0	175	1 CSF3 CANFA	P35834 canis famil
6	738	81.9	174	1 CSF3 SHEEP	O28746 ovis aries
7	727	80.7	195	1 CSF3 BOVIN	F35833 bos taurus
8	702	77.9	195	1 CSF3 PIG	O02837 sus scrofa
9	642	71.3	208	1 CSF3 MOUSE	P09920 mus musculus
10	635	70.5	214	2 P97712	P97712 rattus norv
11	511	56.7	127	2 Q8MKE0	Q8MKE0 equus caball
12	304	33.7	201	1 MGP CHICK	F13854 gallus gall
13	111	12.3	241	2 Q90Y10	Q90Y10 gallus gall
14	110.5	12.3	212	2 Q8MJ75	Q8MJ75 sus scrofa
15	108	12.0	208	2 Q9XT80	Q9XT80 delphinapte
16	106.5	11.8	212	1 IL6 PIG	P26893 sus scrofa
17	101	11.2	205	1 IL6 ORCOR	O28747 orcinus orc
18	100	11.1	208	1 IL6 HORSE	Q95181 equus caball
19	96	10.7	189	2 Q6NZ82	Q6NZ82 homo sapien
20	96	10.7	189	2 Q9HZA5	Q9HZA5 homo sapien
21	96	10.7	189	2 AAH66267	AAH66267 homo sapi
22	95	10.5	208	1 IL6 FELCA	P41683 felis silve
23	94.5	10.5	455	2 Q8D706	Q8D706 vibrio vuln
24	94	10.4	345	2 Q9KTL6	Q9KTL6 vibrio chol
25	93	10.3	189	2 Q9NPF7	Q9NPF7 homo sapien
26	93	10.3	189	2 AAH66268	AAH66268 homo sapi
27	93	10.3	189	2 AAQ89442	AAQ89442 homo sapi
28	93	10.3	189	2 AAH67511	AAH67511 homo sapi
29	93	10.3	189	2 AAH67512	AAH67512 homo sapi
30	93	10.3	189	2 AAH67513	AAH67513 homo sapi
31	91	10.1	189	2 Q6NZ80	Q6NZ80 homo sapien

32	89.5	9.9	189	2 AAH66269	AAH66269 homo sapi
33	89.5	9.9	214	2 Q8MKE5	Q8MKE5 sus scrofa
34	89.5	9.9	2175	1 HMCU DROME	P10180 drosophila
35	88.5	9.8	666	2 Q9A523	Q9A523 caulobacter
36	88.5	9.8	786	2 Q9I019	Q9I019 pseudomonas
37	88.5	9.8	1931	2 Q8RJY3	Q8RJY3 stigmatala
38	88	9.8	290	2 Q9P0S7	Q9P0S7 homo sapien
39	86	9.5	208	1 IL6 BOVIN	P26892 bos taurus
40	86	9.5	502	2 Q34008	Q34008 beta vulgar
41	86	9.5	788	2 Q8CF87	Q8CF87 mus musculu
42	86	9.5	850	2 Q7TQ21	Q7TQ21 mus musculu
43	86	9.5	851	2 Q8CF88	Q8CF88 mus musculu
44	86	9.5	852	2 Q811T9	Q811T9 mus musculu
45	85.5	9.5	211	2 Q865W7	Q865W7 camelus bac

ALIGNMENTS

RESULT 1

ID	Q8N4W3	PRELIMINARY;	PRT;	200 AA.
AC	Q8N4W3;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Colony stimulating factor 3, isoform c.			
GN	Name=CSF3;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RA	Strausberg R.;			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC033245; AAH3245.1; -			
DR	HSSP; P09919; 1GNC.			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0005125; F:cytokine activity; IEA.			
DR	GO; GO:0005138; F:interleukin-6 receptor binding; IEA.			
DR	GO; GO:0006955; P:immune response; IEA.			
DR	InterPro; IPR009079; 4 helix cytokine.			
DR	InterPro; IPR003629; GCSF MGF.			
DR	InterPro; IPR003573; IL6 MGF GCSF.			
DR	InterPro; IPR003574; Interleukin_6.			
DR	Pfam; PF00489; IL6; 1.			
DR	PRINTS; PR00433; IL6GCSFMGF.			

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DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD008388; GCSF MGF; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SW00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 200 AA; 21543 MW; 8648AA5B329A96C CRC64;

Query Match          99.4%; Score 896; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 7.4e-74;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPLGPASSLPQSFLKCLEQVRKIQGDGAALQKLCATYKLCHEBELVLGHSLGIPWAP 61
DB 27 TPLGPASSLPQSFLKCLEQVRKIQGDGAALQKLCATYKLCHEBELVLGHSLGIPWAP 86
QY 62 LSSCPQALQACLSQLHSLGFLYQGLQALGSIPELGPTLDTQLQDVADPATTIWOQ 121
DB 87 LSSCPQALQACLSQLHSLGFLYQGLQALGSIPELGPTLDTQLQDVADPATTIWOQ 146
QY 122 MEELGWAPALQPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 147 MEELGWAPALQPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 200

RESULT 2
CSF3 HUMAN STANDARD; PRT; 207 AA.
AC P09919;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 01-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF) (Pluripoiectin)
DE (Pilgrastim) (Lenograstim).
GN Name=CSF3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86118679; PubMed=3484805;
RA Nagata S., Tsuchiya M., Asano S., Kaziro Y., Yamazaki T., Yamamoto O.,
RA Hirata Y., Kubota N., Oheda M., Nomura H., Ono M.;
RT "Molecular cloning and expression of cDNA for human granulocyte
RT colony-stimulating factor.";
RL Nature 319:415-418 (1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86220137; PubMed=2423327;
RA Nagata S., Tsuchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N.,
RA Oheda M., Nomura H., Yamazaki T.;
RT "The chromosomal gene structure and two mRNAs for human granulocyte
RT colony-stimulating factor.";
RL EMBO J. 5:575-581 (1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87196936; PubMed=3494801;
RA Devlin J.J., Devlin P.E., Myambo K., Lilly M.B., Rado T.A.,
RA Warren M.K.;
RT "Expression of granulocyte colony-stimulating factor by human cell
RT lines.";
RL J. Leukoc. Biol. 41:302-306 (1987).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS MET-157 AND THR-174.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattLESNPS. NHLBI HL66682 program for genomic applications, UW-
RT FHCRS, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 19-207 FROM N.A.
RX MEDLINE=86151684; PubMed=2420009;
RA Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zsebo K.M.,
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RA RA Murdock D.C., Chazin V.R., Bruszewski J., Lu H., Chen K.K.,
RA Barendt J., Platzer E., Moore M.A.S., Mertelsmann R., Welte K.;
RT "Recombinant human granulocyte colony-stimulating factor: effects on
RT normal and leukemic myeloid cells.";
RL Science 232:61-66 (1986).
RN [6]
RX CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=93293942; PubMed=7685769;
RA Clogston C.L., Hu S., Boone T.C., Lu H.S.;
RT "Glycosidase digestion, electrophoresis and chromatographic analysis
RT of recombinant human granulocyte colony-stimulating factor glycoforms
RT produced in Chinese hamster ovary cells.";
RL J. Chromatogr. A 637:55-62 (1993).
RN [7]
RP STRUCTURE BY NMR.
RX MEDLINE=93106200; PubMed=1281794;
RA Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;
RT "Secondary structure of human granulocyte colony-stimulating factor
RT derived from NMR spectroscopy.";
RL FEBS Lett. 314:435-439 (1992).
RN [8]
RP STRUCTURE BY NMR.
RX MEDLINE=94304859; PubMed=7518249;
RA Zink T., Ross A., Luers K., Cieslar C., Rudolph R., Holak T.A.;
RT "Structure and dynamics of the human granulocyte colony-stimulating
RT factor determined by NMR spectroscopy. Loop mobility in a four-helix-
RT bundle protein.";
RL Biochemistry 33:8453-8463 (1994).
RN [9]
RX X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=93281718; PubMed=7685117;
RA Hill C.P., Osslund T.D., Eisenberg D.;
RT "The structure of granulocyte-colony-stimulating factor and its
RT relationship to other growth factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171 (1993).
CC -!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoID=P09919-1; Sequence=Displayed;
CC Name=Short;
CC IsoID=P09919-2; Sequence=VSP 002673;
CC -!- PTM: O-glycan consists of Gal-GalNAc disaccharide which can be
CC modified with up to two sialic acid residues (done in
CC recombinantly expressed G-CSF from CHO cells).
CC -!- PHARMACEUTICAL: Available under the names Neupogen or Granulokine
CC (Amgen/Roche) and Granocyte (Rhône-Poulenc). Used to treat
CC neutropenia (a disorder characterized by an extremely low number
CC of neutrophils in blood).
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC -!- CAUTION: Ref.4 misquotes the gene name as "CSF1".
CC -!- DATABASE: NAME=Neupogen/Granulokine;
CC NOTE=Clinical information on Neupogen/Granulokine;
CC WWW="http://www.neupogen.com/";
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X03438; CAA27168.1; -
CC EMBL; M13008; AAA03056.1; -
CC EMBL; X03656; CAA27291.1; -
CC EMBL; X03655; CAA27290.1; -
CC DR
CC DR
CC DR
CC DR
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DR EMBL; AF388025; AAK62469.1; -.
DR EMBL; M17706; AAA35882.1; -.
DR PIR; A24573; FQUGL.
DR PDB; 1CD9; X-ray; A/C=30-207.
DR PDB; 1GNC; NMR; @=30-207.
DR PDB; 1PGR; X-ray; A/C/E/G=30-207.
DR PDB; 1RHG; X-ray; A/B/C=31-207.
DR Genew; HGNC:2438; CSF3.
DR MIM; 138970; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005130; F:granulocyte colony-stimulating factor recep. . .; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW 3D-structure; Alternative splicing; Cytokine; Glycoprotein;
KW Growth factor; Pharmaceutical; Polymorphism; Signal.
FT SIGNAL 1 30 Granulocyte colony-stimulating factor.
FT CHAIN 31 207
FT DISULFID 69 75
FT DISULFID 97 107
FT CARBOHYD 166 166
FT VARSPIC 66 68
FT VARIANT 157 157
FT VARIANT 174 174
FT HELIX 41 65
FT HELIX 69 71
FT HELIX 77 86
FT TURN 87 88
FT HELIX 105 124
FT TURN 125 127
FT TURN 130 132
FT HELIX 133 156
FT TURN 157 158
FT HELIX 176 203
FT TURN 204 204
SQ SEQUENCE 207 AA; 22293 MW; 421F635ECC776996 CRC64;
Query Match 98.2%; Score 884.5; DB 1; Length 207;
Best Local Similarity 98.3%; Pred. No. 8,7e-73;
Matches 174; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 2 TPLGPASSLPQSFLKCLEQVRKIQGDGAALQEKLVSECATYKLCHEPELVLLGHSIGIP 58
DB 31 TPLGPASSLPQSFLKCLEQVRKIQGDGAALQEKLVSECATYKLCHEPELVLLGHSIGIP 90
QY 59 WAPLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADPATTI 118
DB 91 WAPLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADPATTI 150
QY 119 WQMEELGMAPALQPTQGMAMPASAFQRRAGGVLVASHLQSFLEVSRYVRLHQAOP 175
DB 151 WQMEELGMAPALQPTQGMAMPASAFQRRAGGVLVASHLQSFLEVSRYVRLHQAOP 207
RESULT 3
CSF3_FELCA STANDARD; PRT; 194 AA.
AC 002708;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF) (Fragment).
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GN OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=European shorthair; TISSUE=Lung;
RX MEDLINE=21389237; PubMed=11497496; DOI=10.1006/cyto.2001.0910;
RA Dunham S.P., Onions D.E.;
RT "Isolation, nucleotide sequence and expression of a cDNA encoding
RL Cytokine 14:347-351(2001).
CC CC -!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PFM: O-glycosylated (By similarity).
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; Y08538; CAA69853.1; -.
DR PIR; T09255; T09255.
DR HSSP; P0919; 1RHG.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT NON_TER 1 1
FT SIGNAL <1 20 Potential.
FT CHAIN 21 194 Granulocyte colony-stimulating factor.
FT DISULFID 56 62 By similarity.
FT DISULFID 84 94 By similarity.
FT CARBOHYD 153 153 O-linked (GalNAc... ) (By similarity).
SQ SEQUENCE 194 AA; 21154 MW; F72B7AB3DAE7385E CRC64;
Query Match 82.6%; Score 744; DB 1; Length 194;
Best Local Similarity 81.0%; Pred. No. 5.8e-60;
Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
QY 2 TPLGPASSLPQSFLKCLEQVRKIQGDGAALQEKLVSECATYKLCHEPELVLLGHSIGIPWAP 61
DB 21 TPLGPASSLPQSFLKCLEQVRKIQGDGAALQEKLVSECATYKLCHEPELVLLGHSIGIPWAP 80
QY 62 LSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADPATTIQQ 121
DB 81 LSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADPATTIQQ 140
QY 122 MEELGMAPALQPTQGMAMPASAFQRRAGGVLVASHLQSFLEVSRYVRLHQAOP 175
DB 141 MEDVGMAPAVPPTQGTMTFTSAFQRRAGGVLVASHLQSFLEVSRYVRLHQAOP 194
RESULT 4
Q9GUUO PRELIMINARY; PRT; 195 AA.
ID Q9GUUO
```



```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  MEDLINE=95102116; PubMed=7528579;
RA  O'Brien P.M., Seow H.F., Rothel J.S., Wood P.R.;
RT  "Cloning and sequencing of an ovine granulocyte colony-stimulating
RL  factor cDNA.";
RT  DNA Seq. 4:339-342(1994).
CC  -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC  cytokines that act in hematopoiesis by controlling the production,
CC  differentiation, and function of 2 related white cell populations
CC  of the blood, the granulocytes and the monocytes-macrophages. This
CC  CSF induces granulocytes (By similarity).
CC  -1- SUBUNIT: Monomer.
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- PTM: O-glycosylated (By similarity).
CC  -1- SIMILARITY: Belongs to the IL-6 superfamily.
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; L07939; AAA68006.1; -.
DR  PIR; T10268; T10268.
DR  HSSP; P09919; IRHG.
DR  InterPro; IPR009079; 4 helix cytokine.
DR  InterPro; IPR003629; GCSF MGF.
DR  InterPro; IPR003573; IL6_MGF_GCSF.
DR  Pfam; PF00489; IL6; 1.
DR  PRINTS; PR00433; IL6GCSFMGF.
DR  ProDom; PD008388; GCSF MGF; 1.
DR  SMART; SM00126; IL6; 1.
DR  PROSITE; PS00254; INTERLEUKIN_6; 1.
KW  Cytokine; Glycoprotein; Growth factor.
FT  DISULFID 36 42 By similarity.
FT  DISULFID 64 74 By similarity.
FT  CARBOHYD 133 133 O-linked (GalNAc...) (By similarity).
SQ  SEQUENCE 174 AA; 18806 MW; BA5A8P8D23ACDIE CRC64;

Query Match 81.9%; Score 738; DB 1; Length 174;
Best Local Similarity 82.2%; Pred. No. 1.8e-59;
Matches 143; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 2 TPLGPASSLPQSFLKLCLEQVRKIQGDGAALQKLCATYKLCHEPELVLLGHSLGIPWAP 61
DB 1 TPLGPARSUPQSFLKLCLEQVRKIQADGAELQERLCATHKLCHEPELVLLGHSLGIPQAP 60

QY 62 LSSCPSQALQAGCLSQLHSGFLYQGLLQALAGISPELGPTLDTLQLDVADPATTIWOQ 121
DB 61 LSSCPSQSILQTSCLQDLHGFLYQGLLQALAGISPELAPTLDLTQLDVTDPATTIWLQ 120

QY 122 MEELGMAPALQPTQGMHPAFASFORRAGVLVASHLQSFLEVSVYRVLRLHQAQ 175
DB 121 MEDLGVAQVQPTQGTMTPTSAFORRAGVLVASQLRFLGLAYRGLRYLAEP 174

RESULT 7
CSF3_BOVIN STANDARD; PRT; 195 AA.
ID CSF3_BOVIN
AC P35833; Q9TV89;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN Name=CSF3; Synonyms=GCSF;
OS Bos taurus (Bovine).
OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Holstein;
RA  Heidari M., Kehrl M.B. Jr.;
RT  "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte
RL  colony stimulating factor.";
RT  Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC  [2]
RN  X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RP  MEDLINE=94076341; PubMed=7504736;
RA  Lovejoy B., Cascio D., Eisenberg D.;
RT  "Crystal structure of canine and bovine granulocyte-colony stimulating
RT  factor (G-CSF).";
RL  J. Mol. Biol. 234:640-653(1993).
CC  -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC  cytokines that act in hematopoiesis by controlling the production,
CC  differentiation, and function of 2 related white cell populations
CC  of the blood, the granulocytes and the monocytes-macrophages. This
CC  CSF induces granulocytes.
CC  -1- SUBUNIT: Monomer.
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- PTM: O-glycosylated.
CC  -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; AF092533; AAD16102.1; -.
DR  PDB; 1BGC; X-ray; @=22-195.
DR  InterPro; IPR009079; 4 helix cytokine.
DR  InterPro; IPR003629; GCSF MGF.
DR  InterPro; IPR003573; IL6_MGF_GCSF.
DR  Pfam; PF00489; IL6; 1.
DR  PRINTS; PR00433; IL6GCSFMGF.
DR  ProDom; PD008388; GCSF MGF; 1.
DR  SMART; SM00126; IL6; 1.
DR  PROSITE; PS00254; INTERLEUKIN_6; 1.
KW  3D-structure; Cytokine; Glycoprotein; Growth factor; Signal.
FT  SIGNAL 1 21 Potential.
FT  CHAIN 22 195 Granulocyte colony-stimulating factor.
FT  DISULFID 57 63
FT  DISULFID 85 95
FT  CARBOHYD 154 154
FT  CONFLICT 93 94
FT  HELIX 32 60
FT  HELIX 65 69
FT  TURN 70 71
FT  HELIX 72 75
FT  TURN 76 76
FT  HELIX 83 85
FT  TURN 87 89
FT  HELIX 92 112
FT  TURN 113 115
FT  TURN 118 120
FT  HELIX 121 145
FT  HELIX 164 191
FT  TURN 192 192
SQ  SEQUENCE 195 AA; 21431 MW; 8C06119E4ADFBA73 CRC64;

Query Match 80.7%; Score 727; DB 1; Length 195;
Best Local Similarity 81.0%; Pred. No. 2.1e-58;
Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 2 TPLGPASSLPQSFLKLCLEQVRKIQGDGAALQKLCATYKLCHEPELVLLGHSLGIPWAP 61
DB 22 TPLGPARSUPQSFLKLCLEQVRKIQADGAELQERLCATHKLCHEPELVLLGHSLGIPQAP 81

QY 62 LSSCPSQALQAGCLSQLHSGFLYQGLLQALAGISPELGPTLDTLQLDVADPATTIWOQ 121
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Db 82 LSSCSQSLSLCLNQLHGLFLVQLLQALAGISPELAPLDTLQLDVDFATNIWLQ 141
QY 122 MEELGNAPALQTOGAMPAFASAFORRAGGVLVASHQSFLFVSFVRLVHLAQP 175
Db 142 MEDLGAAPAVQTOGAMPFTTSAFORRAGGVLVASQLHRFLEFLAYRGLRYLAEP 195

RESULT 8

CSF3_PIG STANDARD; PRT; 195 AA.
ID CSF3_PIG
AC 002837; 019180;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN Name=CSF3;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kulmburg P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Gloster S.E.; Sandeman R.M.; Strom A.D.G.;
RT "Cloning of a cDNA and gene encoding porcine granulocyte-colony
stimulating factor.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
cytokines that act in hematopoiesis by controlling the production,
differentiation, and function of 2 related white cell populations
of the blood, the granulocytes and the monocytes-macrophages. This
CSF induces granulocytes (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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CC
CC EMBL; Y10494; CAA71518.1; -;
CC EMBL; U68482; AAB70701.1; -;
CC EMBL; U68481; AAB70700.1; -;
CC HSP; P09919; IRRG.
CC InterPro; IPR009079; 4 helix cytokine.
CC InterPro; IPR003629; GCSF_MGF.
CC InterPro; IPR003573; IL6_MGF_GCSF.
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PRODOM; PD008386; GCSF_MGF; 1.
CC SMART; SM00126; IL6; 1.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
CC Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 195 Granulocyte colony-stimulating factor.
FT DISULFID 57 63 By similarity.
FT DISULFID 85 95 By similarity.
FT CARBOHYD 154 154 O-linked (GalNAc...) (By similarity).
FT CONFLICT 123 123 A -> R (in Ref. 1).
SQ SEQUENCE 195 AA; 21214 MW; 84787P20DB0AEALC CRC64;
Query Match 77.9%; Score 702; DB 1; Length 195;
Best Local Similarity 79.2%; Pred. No. 4.1e-56;

Matches 137; Conservative 11; Mismatches 25; Indels 0; Gaps 0;
QY 3 PLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVVLGHSLGIPWAPL 62
Db 23 PLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVVLGHSLGIPWAPL 82
QY 63 SSCPSQALQALAGCSLSHLSGLFLVQLLQALAGISPELAPLDTLQLDVDFATNIWQOM 122
Db 83 SSCPSQALQALAGCSLSHLSGLFLVQLLQALAGISPELAPLDTLQLDVDFATNIWQOM 142
QY 123 EELGNAPALQTOGAMPAFASAFORRAGGVLVASHQSFLFVSFVRLVHLAQP 175
Db 143 EDLRMAPASLPTQGTPTTSAFORRAGGVLVASHQSFLFVSFVRLVHLAQP 195

RESULT 9

CSF3_MOUSE STANDARD; PRT; 208 AA.
ID CSF3_MOUSE
AC P09920;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN Name=Csfg; Synonyms=Csf3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=87017003; PubMed=3489940;
RT Tsuchiya M., Asano S., Kaziro Y., Nagata S.;
RT "Isolation and characterization of the cDNA for murine granulocyte
colony-stimulating factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:7633-7637(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=87190474; PubMed=3494605;
RT Tsuchiya M., Kaziro Y., Nagata S.;
RT "The chromosomal gene structure for murine granulocyte colony-
stimulating factor.";
RL Eur. J. Biochem. 165:7-12(1987).
RN [3]
RP PARTIAL SEQUENCE.
RA Simpson R.J., Nice E.C., Nicola N.A.;
RT "Structural studies on the murine granulocyte colony-stimulating
factor.";
RL Biol. Chem. Hoppe-Seyler 368:1327-1331(1987).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
cytokines that act in hematopoiesis by controlling the production,
differentiation, and function of 2 related white cell populations
of the blood, the granulocytes and the monocytes-macrophages. This
CSF induces granulocytes.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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CC
CC EMBL; M13926; AAA37672.1; -;
CC EMBL; X05402; CAA28986.1; -;
CC PIR; A29536; A26496.
CC HSP; P09919; IRRG.
CC MGI; 1339751; Csf3.
CC InterPro; IPR009079; 4_helix_cytokine.
CC

```
DR InterPro; IPR003629; GCSF_MGF
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Direct protein sequencing; Glycoprotein; Growth factor;
KW SIGNAL.
FT CHAIN 1 30 Granulocyte colony-stimulating factor.
FT DISULFID 31 208 By similarity.
FT DISULFID 72 78 By similarity.
FT DISULFID 100 110 By similarity.
FT CARBOHYD 169 169 O-linked (GlcNAc...) (By similarity).
SQ SEQUENCE 208 AA; 22421 MW; 0BF3622135C906DB CRC64;

Query Match 71.3%; Score 642; DB 1; Length 208;
Best Local Similarity 74.6%; Pred. No. 1.4e-50;
Matches 129; Conservative 11; Mismatches 33; Indels 0; Gaps 0;

QY 1 MTPGLPASSLPQSLKLEQVRKIQDGAALQEKLCATYKLCBPBELVLLGHSIGIPWA 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 36 VSAIPSPSLPLPSFLKSLKLEQVRKIQASGSVLLQELCATYKLCBPBELVLLGHSIGIPKA 95

QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLQALLEGISPELPTDLDVADVFATTIQ 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 96 SLSSGSSQALQQTCKLSQLHSGFLYQGLQALLEGISPELPTDLDVADVFATTIQ 155

QY 121 QMEELGMAPALQPTQGMAPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLA 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 156 QMENLGAVTQPTQGMAPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLA 208

RESULT 10
P97712 PRELIMINARY; PRT; 214 AA.
AC P97712;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
DE Granulocyte colony stimulating factor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97074656; PubMed-8917083;
RA Han S.W., Ramesh N., Osborne W.R.;
RT "Cloning and expression of the cDNA encoding rat granulocyte colony-
   stimulating factor."
RL Gene 175:101-104(1996).
DR EMBL; U37101; AAC52915.1; -.
DR PIR; JC5043; JC5043.
DR HSSP; P09919; IRHG.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 214 AA; 23659 MW; 29BB88B17B684C55 CRC64;

Query Match 70.5%; Score 635; DB 2; Length 214;
Best Local Similarity 72.6%; Pred. No. 6.1e-50;
Matches 127; Conservative 12; Mismatches 36; Indels 0; Gaps 0;

DR InterPro; IPR003629; GCSF_MGF
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 214 AA; 23659 MW; 29BB88B17B684C55 CRC64;

Query Match 70.5%; Score 635; DB 2; Length 214;
Best Local Similarity 72.6%; Pred. No. 6.1e-50;
Matches 127; Conservative 12; Mismatches 36; Indels 0; Gaps 0;

QY 1 MTPGLPASSLPQSLKLEQVRKIQDGAALQEKLCATYKLCBPBELVLLGHSIGIPWA 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 36 VSAIPSPSLPLPSFLKSLKLEQVRKIQASGSVLLQELCATYKLCBPBELVLLGHSIGIPKA 95

QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLQALLEGISPELPTDLDVADVFATTIQ 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 96 SLSSGSSQALQQTCKLSQLHSGFLYQGLQALLEGISPELPTDLDVADVFATTIQ 155

QY 121 QMEELGMAPALQPTQGMAPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLA 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 156 QMENLGAVTQPTQGMAPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLA 208

RESULT 11
Q8MKEO PRELIMINARY; PRT; 127 AA.
AC Q8MKEO;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
DE Granulocyte colony-stimulating factor.
GN Name=G-CSF;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Noronha L.E., Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF503365; AM34205.1; -.
DR HSSP; P09919; IRHG.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 127 AA; 13657 MW; 25559C2569802077 CRC64;

Query Match 56.7%; Score 511; DB 2; Length 127;
Best Local Similarity 79.5%; Pred. No. 7.7e-39;
Matches 101; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 49 VLLGHSIGIPWAPLSSCPQALQAGCLSQLHSGFLYQGLQALLEGISPELPTDLDV 108
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MLGHSIGIPQPLSSCPQALQAGCLSQLHSGFLYQGLQALLEGISPELPTDLDV 60

QY 109 LDVADVFATTIQMEELGMAPALQPTQGMAPAFASAFORRAGGVVASHLQSFLEVSRYV 168
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 LDVADVFATTIQMEELGMAPALQPTQGMAPAFASAFORRAGGVVASHLQSFLEVSRYV 120

QY 169 LRHLAQP 175
   : : : : :
Db 121 LRHLAEP 127

RESULT 12
MGF_CHICK
ID_MGF_CHICK STANDARD; PRT; 201 AA.
AC P13854;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Myelomonocytic growth factor precursor (MGF).
OC Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:11:24 ; Search time 63.5 Seconds
(without alignments)
988.624 Million cell updates/sec

Title: 10032108-2EDIT

Perfect score: 901

Sequence: 1 MTPGLPASSLPQSFLLRCLE.....SHLQSFLEVSRYVRLHLAQP 175

Scoring table: BLASUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	901	100.0	175	2	AAR56558 G-CSF ana
2	898	99.7	175	2	AAR56560 G-CSF ana
3	896	99.4	174	7	ADK41237 Human gra
4	896	99.4	348	5	ABG32031 Single ch
5	895	99.3	175	2	AAR56555 G-CSF ana
6	895	99.3	175	2	AAR56553 G-CSF ana
7	895	99.3	175	2	AAR56559 G-CSF ana
8	895	99.3	175	2	AAR56557 G-CSF ana
9	895	99.3	175	2	AAR56556 G-CSF ana
10	893	99.1	348	5	ABG32030 Single ch
11	892	99.0	175	1	AAP71030 Sequence
12	892	99.0	175	1	AAP70732 Sequence
13	892	99.0	175	1	AAP90107 Human gra
14	892	99.0	175	1	AAP90170 Human gra
15	892	99.0	175	1	AAP91070 Human gra
16	892	99.0	175	2	AAR56555 Platelet
17	892	99.0	175	2	AAR56553 Recombina
18	892	99.0	175	2	AAR56559 PEGylated
19	892	99.0	175	2	AAR56557 Human gra
20	892	99.0	175	3	AAY78936 Granulocyte
21	892	99.0	175	3	AAB14851 Human gra
22	892	99.0	175	3	AAY97017 Mature gr
23	892	99.0	175	3	AAB23758 Human gra
24	892	99.0	175	4	AAG67563 Amino aci
25	892	99.0	175	4	AAG67502 Amino aci

26	892	99.0	175	4	AAR56558	AAR56558 standard; protein; 175 AA.
27	892	99.0	175	4	AAR56558	
28	892	99.0	175	4	AAR56558	
29	892	99.0	175	5	AAR56558	
30	892	99.0	175	6	AAR56558	
31	892	99.0	175	8	AAR56558	
32	892	99.0	175	2	AAR56558	
33	890	98.8	174	7	ADK41238	
34	890	98.8	174	7	ADK41238	
35	890	98.8	174	7	ADK41238	
36	890	98.8	348	5	ABG32029	
37	889	98.7	175	2	AAR56552	
38	889	98.7	175	2	AAR56555	
39	889	98.7	175	2	AAR56578	
40	889	98.7	175	2	AAR56569	
41	889	98.7	175	2	AAR56586	
42	889	98.7	175	2	AAR56554	
43	889	98.7	175	2	AAR56579	
44	889	98.7	759	8	ADL16718	
45	889	98.7	783	2	AAR39473	

ALIGNMENTS

RESULT 1

AAR56558

ID AAR56558 standard; protein; 175 AA.

XX AAR56558;

AC AAR56558;

XX AAR56558;

DT 25-MAR-2003 (revised)

DT 21-MAR-1995 (first entry)

XX G-CSF analogue, K17,35,41>R17,35,41.

XX Granulocyte colony stimulating factor; G-CSF; 3-D structure; mutagenic; hydrophobic; hydrophilic; resistant; proteolysis; activity; antagonist.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "May be absent"

FT Misc-difference 17 /label= K17R

FT Misc-difference 35 /label= K35R

FT Misc-difference 41 /label= K41R

FT WO9417185-A1.

PD 04-AUG-1994.

XX 25-JAN-1994; 94WO-US0000913.

XX 28-JAN-1993; 93US-00010099.

XX (AMGE-) AMGEN INC.

XX Osslund TD;

XX WPI; 1994-264099/32.

XX Granulocyte colony stimulating factor analogues - with altered, biological activity, identified by analysis of three-dimensional structure of native protein.

XX Claim 21; Page 96; 206pp; English.

XX The sequences given in AAR56553-96 represent analogues of granulocyte colony stimulating factor (G-CSF). These analogues contain at least one

CC changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed
 CC mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The
 CC amino acids which were to be changed were determined by displaying the 3-
 CC D structure of G-CSF on a computer. It is now possible to predict
 CC accurately how changes in G-CSF structure will alter the characteristics
 CC of the protein, particularly hydrophobic and hydrophilic areas can be
 CC characterised. These new analogues have controllably altered properties,
 CC eg. better resistance to proteolysis, higher or lower activity, including
 CC no hematopoietic at all, ie. antagonists, longer shelf, easier
 CC formulation etc. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 175 AA;

Query Match 100.0%; Score 901; DB 2; Length 175;
 Best Local Similarity 100.0%; Pred. No. 2.7e-90;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGPAASLPQSFLRLCLQEVKRIQGDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
 Db 1 MTPLGPAASLPQSFLRLCLQEVKRIQGDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
 QY 61 PLSSCPQALQAGCLSQLHSLGLFYQGLLQALEGISPELGTDLTQLDVAADFATTIWO 120
 Db 61. PLSSCPQALQAGCLSQLHSLGLFYQGLLQALEGISPELGTDLTQLDVAADFATTIWO 120
 QY 121 QMEELGMALPQTOGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 Db 121 QMEELGMALPQTOGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 2
 AAR56560
 ID AAR56560 standard; protein; 175 AA.
 XX
 AC AAR56560;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-MAR-1995 (first entry)
 XX
 DE G-CSF analogue, K17,24,35,41>R17,24,35,41.
 XX
 KW Granulocyte colony stimulating factor; G-CSF; 3-D structure; mutagenic;
 KW hydrophobic; hydrophilic; resistant; proteolysis; activity; antagonist.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 1 /note= "May be absent"
 FT Misc-difference 17 /label= K17R
 FT Misc-difference 24 /label= K24R
 FT Misc-difference 35 /label= K35R
 FT Misc-difference 41 /label= K41R
 FT
 XX

PN WO9417185-A1.
 XX
 PD 04-AUG-1994.
 XX
 PF 25-JAN-1994; 94WO-US000913.
 XX
 PR 28-JAN-1993; 93US-00010099.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Oselund TD;
 XX
 DR WPI; 1994-264099/32.
 XX

PT Granulocyte colony stimulating factor analogues - with altered,
 PT biological activity, identified by analysis of three-dimensional
 PT structure of native protein.

XX Claim 23; Page 98; 206pp; English.

XX The sequences given in AAR56553-96 represent analogues of granulocyte
 CC colony stimulating factor (G-CSF). These analogues contain at least one
 CC changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed
 CC mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The
 CC amino acids which were to be changed were determined by displaying the 3-
 CC D structure of G-CSF on a computer. It is now possible to predict
 CC accurately how changes in G-CSF structure will alter the characteristics
 CC of the protein, particularly hydrophobic and hydrophilic areas can be
 CC characterised. These new analogues have controllably altered properties,
 CC eg. better resistance to proteolysis, higher or lower activity, including
 CC no hematopoietic at all, ie. antagonists, longer shelf, easier
 CC formulation etc. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PI field.)
 XX

XX Sequence 175 AA;

Query Match 99.7%; Score 898; DB 2; Length 175;
 Best Local Similarity 99.4%; Pred. No. 5.7e-90;
 Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGPAASLPQSFLRLCLQEVKRIQGDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
 Db 1 MTPLGPAASLPQSFLRLCLQEVKRIQGDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
 QY 61 PLSSCPQALQAGCLSQLHSLGLFYQGLLQALEGISPELGTDLTQLDVAADFATTIWO 120
 Db 61 PLSSCPQALQAGCLSQLHSLGLFYQGLLQALEGISPELGTDLTQLDVAADFATTIWO 120
 QY 121 QMEELGMALPQTOGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 Db 121 QMEELGMALPQTOGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 3
 ADK41237
 ID ADK41237 standard; protein; 174 AA.
 XX
 AC ADK41237;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human granulocyte colony-stimulating factor mutant, K16R+K34R+K40R.

XX granulocyte colony-stimulating factor; G-CSF; immunostimulant; anti-HIV;
 KW virucide; antibacterial; fungicide; cytostatic; neutropenia; leukopenia;
 KW chemotherapy; radiation therapy; HIV; AIDS; immunodeficiency disease;
 KW bacterial infection; acute myeloid leukaemia; antifungal therapy;
 KW systemic; invasive candidiasis; human; hG-CSF; mutant; mutein.

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 16 /note= "The wild-type residue was substituted with Arg"
 FT Misc-difference 34 /note= "The wild-type residue was substituted with Arg"
 FT Misc-difference 40 /note= "The wild-type residue was substituted with Arg"
 XX

PN WO2003006501-A2.
 XX
 PD 23-JAN-2003.
 XX
 PF 10-JUL-2002; 2002WO-DK000482.
 XX
 PR 11-JUL-2001; 2001US-00904196.

PR 22-MAR-2002; 2002DK-00000447.
XX 08-MAY-2002; 2002DK-00000708.
XX (MAXY-) MAXYGEN HOLDINGS LTD.
XX Nissen TL, Andersen KV, Hansen CK, Mikkelsen JM, Schambye HT;
XX WPI; 2003-221717/21.
XX New polypeptide conjugate exhibiting granulocyte colony-stimulating
XX factor activity, useful for preventing or treating neutropenia or
XX leucopenia due to chemotherapy or radiation therapy, AIDS or other
XX immunodeficiency diseases.
XX Claim 6; Page: 106pp; English.
XX The invention relates to a novel polypeptide conjugate exhibiting
XX granulocyte colony-stimulating factor activity (G-CSF). The polypeptide
XX conjugate comprises: a polypeptide comprising at least one substitution
XX selected from the group of K16R/Q, K34R/Q, and K40R/Q, and at least one
XX substitution selected from the group of T105K and S159K relative to the
XX amino acid sequence of hG-CSF having a 174 residue amino acid sequence,
XX given in the specification, or in a corresponding position relative to an
XX amino acid sequence having at least 80 % sequence identity with the 174
XX residue amino acid sequence, where the conjugate has 2-6 polyethylene
XX glycol moieties with a molecular weight of 1000-10000 Da attached to
XX attachment groups of the polypeptide; or a polypeptide comprising an
XX amino acid sequence that differs in at least one amino acid residue from
XX the amino acid sequence of hG-CSF having the sequence of the 174 residue
XX amino acid sequence, and with at least one non-polypeptide moiety
XX attached to an attachment group of the polypeptide, where the conjugate
XX has an in vitro bioactivity in the range of 2-30% of the bioactivity of
XX non-conjugated hG-CSF as determined by the luciferase assay. The G-CSF
XX conjugate has immunostimulant, anti-HIV, virucide, antibacterial,
XX fungicide, and cytostatic activities. The polypeptide conjugate is useful
XX as a pharmaceutical, or for preparing a pharmaceutical composition for
XX treating an insufficient neutrophil level. The pharmaceutical composition
XX is also useful for preventing and/or treating neutropenia or leukopenia
XX due to chemotherapy or radiation therapy, or due to HIV or another viral
XX infection. The polypeptide conjugate may also be used for treating AIDS
XX or other immunodeficiency diseases, bacterial infections, acute myeloid
XX leukaemia, or for antifungal therapy, particularly for treating systemic
XX or invasive candidiasis. This sequence represents a mutant human G-CSF
XX protein of the invention. Note: This sequence is not shown in the
XX specification. It has been created from the wild-type human G-CSF protein
XX sequence ADK41219 and from information provided in the claims.
XX Sequence 174 AA;
SQ Query Match 99.4%; Score 896; DB 7; Length 174;
Best Local Similarity 100.0%; Pred. No. 9.3e-90;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TPLGPASSLPQSFLLRCLQSVKRIQGDGAALQERLCATYRLCHPELVLLHSLGIPWAP 61
Db 1 TPLGPASSLPQSFLLRCLQSVKRIQGDGAALQERLCATYRLCHPELVLLHSLGIPWAP 60
QY 62 LSSCPQALQALGCLSQLHSLFLYQGLQALGEGISPELGPTLDTLQDVADPATTIWOQ 121
Db 61 LSSCPQALQALGCLSQLHSLFLYQGLQALGEGISPELGPTLDTLQDVADPATTIWOQ 120
QY 122 MBEELGNAPALQPTQGAAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
Db 121 MBEELGNAPALQPTQGAAPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 174
RESULT 4
ID ABG32031
XX ABG32031 standard; protein; 348 AA.
AC ABG32031;
XX
XX 15-NOV-2002 (first entry)
DT

XX Single chain G-CSF dimer polypeptide mutant, #3.
DE Single-chain multimeric polypeptide; polyethylene glycol; PEG;
XX granulocyte colony stimulating factor; G-CSF; human;
KW haematopoietic disorder; radiation therapy; chemotherapy;
KW bone marrow transplantation; acquired immunodeficiency syndrome; AIDS;
KW immunodeficiency disease; leukopenia; acute myeloid leukaemia; half-life;
KW clearance; immunogenicity; bioavailability; single chain G-CSF dimer;
KW antihuman immunodeficiency virus; HIV; haemostatic; mutant; mutein.
XX Homo sapiens.
OS Synthetic.
OS
XX Key Location/Qualifiers
FH 1. .174
FT Region /note= "This region is copy 1 of the monomeric G-CSF
FT polypeptide encoded by either ABS52516 or ABS52519"
FT Misc-difference 16 /note= "Wild-type Lys substituted by Arg"
FT Misc-difference 34 /note= "Wild-type Lys substituted by Arg"
FT Misc-difference 40 /note= "Wild-type Lys substituted by Arg"
FT Region /note= "Wild-type Lys substituted by Arg"
FT 175. .348
FT /note= "This region is copy 2 of the monomeric G-CSF
FT polypeptide encoded by ABS52517"
FT Misc-difference 190 /note= "Wild-type Lys substituted by Arg"
FT Misc-difference 208 /note= "Wild-type Lys substituted by Arg"
FT Misc-difference 214 /note= "Wild-type Lys substituted by Arg"
FT /note= "Wild-type Lys substituted by Arg"
XX WO200236626-A1.
XX 10-MAY-2002.
XX 01-NOV-2001; 2001WO-DK000724.
XX 02-NOV-2000; 2000DK-00001647.
XX (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX Nissen TL, Jensen AD;
XX WPI; 2002-618972/66.
XX Single chain multimeric polypeptide conjugate for treating hematopoietic
PT disorders, has two units of monomeric polypeptides linked via peptide
PT bond/linker and polymer group bound to attachment group of polypeptide.
XX Example 7; Page: 108pp; English.
XX The invention discloses a single-chain multimeric polypeptide conjugate
XX comprising at least two units of a monomeric polypeptide linked via a
XX peptide bond or a peptide linker, where the monomeric polypeptide is
XX biologically active in its monomeric form and has at least one polymer
XX group covalently bound to an attachment group of the polypeptide e.g.
XX polyethylene glycol (PEG). The polypeptide is preferably a single-chain
XX multimeric granulocyte colony stimulating factor (G-CSF) polypeptide
XX comprising at least two G-CSF polypeptide monomers, linked via a peptide
XX bond or a peptide linker, where at least one of the monomers is a variant
XX of wild-type human G-CSF comprising at least one amino acid residue
XX modification. The monomeric and multimeric polypeptides are useful in
XX therapy and for manufacture of a medicament for treatment of general
XX haematopoietic disorders, including disorders arising from radiation
XX therapy, chemotherapy or bone marrow transplantations, acquired
XX immunodeficiency syndrome (AIDS) or other immunodeficiency diseases,
XX leukopenia and acute myeloid leukaemia. The conjugate has one or more
XX important properties as compared to the native polypeptide, including
XX increased functional in vivo half-life, increased serum half-life,

CC reduced clearance, reduced immunogenicity and/or increased
 CC bioavailability. Consequently, medical treatment with a conjugate offers
 CC advantages including longer duration between injections and fewer side
 CC effects. The sequence presented is the single chain G-CSF dimer
 CC polypeptide mutant, #3. Note: This sequence was not shown in the
 CC specification but was created by the indexer from information given in
 CC example 7
 XX
 CC Sequence 348 AA;

Query Match 99.4%; Score 896; DB 5; Length 348;
 Best Local Similarity 100.0%; Pred. No. 2.3e-89;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPLGPASSLPQSFLRLCLQVQRKIQDGAALQERLCATYRLCHPELVLLGSLGIPWAP 61
 DB 1 TPLGPASSLPQSFLRLCLQVQRKIQDGAALQERLCATYRLCHPELVLLGSLGIPWAP 60
 QY 62 LSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWO 121
 DB 61 LSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWO 120
 QY 122 MEELGMAPALOPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRLHAQP 175
 DB 121 MEELGMAPALOPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRLHAQP 174

RESULT 5
 AAR56555
 ID AAR56555 standard; protein; 175 AA.
 XX
 AC AAR56555;
 DT 25-MAR-2003 (revised)
 DT 21-MAR-1995 (first entry)
 DE G-CSF analogue, K35R.
 XX
 KW Granulocyte colony stimulating factor; G-CSF; 3-D structure; mutagenic;
 KW hydrophobic; hydrophilic; resistant; proteolysis; activity; antagonist.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "May be absent"
 FT Misc-difference 35 /label= K35R
 FT
 XX WO9417185-A1.
 PN
 XX
 PD 04-AUG-1994.
 XX
 PF 25-JAN-1994; 94WO-US000913.
 XX
 PR 28-JAN-1993; 93US-00010099.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Oeslund TD;
 PI
 XX WPI; 1994-264099/32.
 DR
 XX Granulocyte colony stimulating factor analogues - with altered,
 PT biological activity, identified by analysis of three-dimensional
 PT structure of native protein.
 XX
 XX Claim 18; Page 94; 206pp; English.
 PS
 XX The sequences given in AAR56553-96 represent analogues of granulocyte
 CC colony stimulating factor (G-CSF). These analogues contain at least one
 CC changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed
 CC mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The

CC amino acids which were to be changed were determined by displaying the 3-
 CC D structure of G-CSF on a computer. It is now possible to predict
 CC accurately how changes in G-CSF structure will alter the characteristics
 CC of the protein, particularly hydrophobic and hydrophilic areas can be
 CC characterised. These new analogues have controllably altered properties,
 CC eg. better resistance to proteolysis, higher or lower activity, including
 CC no hematoopoietic at all, ie. antagonists, longer shelf, easier
 CC formulation etc. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PI field.)
 XX
 CC Sequence 175 AA;

Query Match 99.3%; Score 895; DB 2; Length 175;
 Best Local Similarity 98.9%; Pred. No. 1.2e-89;
 Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLPASSLPQSFLRLCLQVQRKIQDGAALQERLCATYRLCHPELVLLGSLGIPWA 60
 DB 1 MTPLPASSLPQSFLRLCLQVQRKIQDGAALQERLCATYRLCHPELVLLGSLGIPWA 60
 QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWO 120
 DB 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWO 120
 QY 121 QMEELGMAPALOPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRLHAQP 175
 DB 121 QMEELGMAPALOPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRLHAQP 175

RESULT 6
 AAR56553
 ID AAR56553 standard; protein; 175 AA.
 XX
 AC AAR56553;
 DT 25-MAR-2003 (revised)
 DT 21-MAR-1995 (first entry)
 DE G-CSF analogue, K17R.
 XX
 KW Granulocyte colony stimulating factor; G-CSF; 3-D structure; mutagenic;
 KW hydrophobic; hydrophilic; resistant; proteolysis; activity; antagonist.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "May be absent"
 FT Misc-difference 17 /label= K17R
 FT
 XX WO9417185-A1.
 PN
 XX
 PD 04-AUG-1994.
 XX
 PF 25-JAN-1994; 94WO-US000913.
 XX
 PR 28-JAN-1993; 93US-00010099.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Oeslund TD;
 PI
 XX WPI; 1994-264099/32.
 DR
 XX Granulocyte colony stimulating factor analogues - with altered,
 PT biological activity, identified by analysis of three-dimensional
 PT structure of native protein.
 XX
 XX Claim 17; Page 92; 206pp; English.
 PS
 XX The sequences given in AAR56553-96 represent analogues of granulocyte
 CC colony stimulating factor (G-CSF). These analogues contain at least one

CC changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed
 CC mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The
 CC amino acids which were to be changed were determined by displaying the 3-
 CC D structure of G-CSF on a computer. It is now possible to predict
 CC accurately how changes in G-CSF structure will alter the characteristics
 CC of the protein, particularly hydrophobic and hydrophilic areas can be
 CC characterised. These new analogues have controllably altered properties,
 CC eg. better resistance to proteolysis, higher or lower activity, including
 CC no hemagglutinating at all, ie. antagonists, longer shelf, easier
 CC formulation etc. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 175 AA;

Query Match 99.3%; Score 895; DB 2; Length 175;
 Best Local Similarity 98.9%; Pred. No. 1.2e-89;
 Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPOSLFLRCLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
 DB 1 MTPLGPASSLPOSLFLRCLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
 QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
 DB 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
 QY 121 QMEELGNAPALQPTQGAAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
 DB 121 QMEELGNAPALQPTQGAAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

RESULT 7

AAR56559
 ID AAR56559 standard; protein; 175 AA.

XX AAR56559;

XX 25-MAR-2003 (revised)

DT 21-MAR-1995 (first entry)

XX G-CSF analogue, K24,35,41>R24,35,41.

XX Granulocyte colony stimulating factor; G-CSF; 3-D structure; mutagenic;
 KW hydrophobic; hydrophilic; resistant; proteolysis; activity; antagonist.
 XX Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 1 /note= "May be absent"
 FT Misc-difference 24 /label= K24R
 FT Misc-difference 35 /label= K35R
 FT Misc-difference 41 /label= K41R

XX WO9417185-A1.

XX 04-AUG-1994.

XX 25-JAN-1994; 94WO-US0000913.

XX 28-JAN-1993; 93US-00010099.

XX (AMGE-) AMGEN INC.

XX Osslund TD;

XX WPI; 1994-264099/32.

XX Granulocyte colony stimulating factor analogues - with altered,
 PT biological activity, identified by analysis of three-dimensional

PT structure of native protein.

XX Claim 22; Page 97; 206pp; English.

XX The sequences given in AAR5653-96 represent analogues of granulocyte
 CC colony stimulating factor (G-CSF). These analogues contain at least one
 CC changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed
 CC mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The
 CC amino acids which were to be changed were determined by displaying the 3-
 CC D structure of G-CSF on a computer. It is now possible to predict
 CC accurately how changes in G-CSF structure will alter the characteristics
 CC of the protein, particularly hydrophobic and hydrophilic areas can be
 CC characterised. These new analogues have controllably altered properties,
 CC eg. better resistance to proteolysis, higher or lower activity, including
 CC no hemagglutinating at all, ie. antagonists, longer shelf, easier
 CC formulation etc. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 175 AA;

Query Match 99.3%; Score 895; DB 2; Length 175;

Best Local Similarity 98.9%; Pred. No. 1.2e-89;

Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPOSLFLRCLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60

DB 1 MTPLGPASSLPOSLFLRCLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60

QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120

DB 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120

QY 121 QMEELGNAPALQPTQGAAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

DB 121 QMEELGNAPALQPTQGAAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

RESULT 8

AAR56557

ID AAR56557 standard; protein; 175 AA.

XX AAR56557;

XX 25-MAR-2003 (revised)

DT 21-MAR-1995 (first entry)

XX G-CSF analogue, K17,24,35>R17,24,35.

XX Granulocyte colony stimulating factor; G-CSF; 3-D structure; mutagenic;
 KW hydrophobic; hydrophilic; resistant; proteolysis; activity; antagonist.
 XX Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 1 /note= "May be absent"
 FT Misc-difference 17 /label= K17R
 FT Misc-difference 24 /label= K24R
 FT Misc-difference 35 /label= K35R

XX WO9417185-A1.

XX 04-AUG-1994.

XX 25-JAN-1994; 94WO-US0000913.

XX 28-JAN-1993; 93US-00010099.

XX (AMGE-) AMGEN INC.

```

PI Osslund TD;
DR WPI; 1994-264099/32.
XX
XX Granulocyte colony stimulating factor analogues - with altered,
PT biological activity, identified by analysis of three-dimensional
PT structure of native protein.
XX
PS Claim 20; Page 95-96; 206pp; English.
XX
CC The sequences given in AAR56553-96 represent analogues of granulocyte
CC colony stimulating factor (G-CSF). These analogues contain at least one
CC changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed
CC mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The
CC amino acids which were to be changed were determined by displaying the 3-
CC D structure of G-CSF on a computer. It is now possible to predict
CC accurately how changes in G-CSF structure will alter the characteristics
CC of the protein, particularly hydrophobic and hydrophilic areas can be
CC characterised. These new analogues have controllably altered properties,
CC eg. better resistance to proteolysis, higher or lower activity, including
CC no hematopoietic at all, ie. antagonists, longer shelf, easier
CC formulation etc. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 175 AA;
Query Match 99.3%; Score 895; DB 2; Length 175;
Best Local Similarity 98.9%; Pred. No. 1.2e-89;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLRLCLLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSLGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSLGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIWO 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIWO 120
QY 121 QMEELGMAPALOPTQGMPPAFASAFQRRAGGVLVASHLQSFLEVSRYRLHRLAQP 175
DB 121 QMEELGMAPALOPTQGMPPAFASAFQRRAGGVLVASHLQSFLEVSRYRLHRLAQP 175

RESULT 9
AAR56556
ID AAR56556 standard; protein; 175 AA.
XX
AC AAR56556;
XX
XX 25-MAR-2003 (revised)
DT 21-MAR-1995 (first entry)
XX
DE G-CSF analogue, K41R.
XX
XX Granulocyte colony stimulating factor; G-CSF; 3-D structure; mutagenic;
KW hydrophobic; hydrophilic; resistant; proteolysis; activity; antagonist.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Key 1
FT Misc-difference 1 /note= "May be absent"
FT Misc-difference 41 /label= K41R
FT
FT
XX WO9417185-A1.
XX
XX 04-AUG-1994.
PD
XX 25-JAN-1994; 94WO-US000913.
PF
XX 28-JAN-1993; 93US-00010099.
PR
XX
XX

```

```

PA (AMGE-) AMGEN INC.
XX
PI Osslund TD;
XX
XX WPI; 1994-264099/32.
DR
XX Granulocyte colony stimulating factor analogues - with altered,
PT biological activity, identified by analysis of three-dimensional
PT structure of native protein.
XX
PS Claim 19; Page 94-95; 206pp; English.
XX
CC The sequences given in AAR56553-96 represent analogues of granulocyte
CC colony stimulating factor (G-CSF). These analogues contain at least one
CC changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed
CC mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The
CC amino acids which were to be changed were determined by displaying the 3-
CC D structure of G-CSF on a computer. It is now possible to predict
CC accurately how changes in G-CSF structure will alter the characteristics
CC of the protein, particularly hydrophobic and hydrophilic areas can be
CC characterised. These new analogues have controllably altered properties,
CC eg. better resistance to proteolysis, higher or lower activity, including
CC no hematopoietic at all, ie. antagonists, longer shelf, easier
CC formulation etc. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 175 AA;
Query Match 99.3%; Score 895; DB 2; Length 175;
Best Local Similarity 98.9%; Pred. No. 1.2e-89;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLRLCLLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSLGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSLGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIWO 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIWO 120
QY 121 QMEELGMAPALOPTQGMPPAFASAFQRRAGGVLVASHLQSFLEVSRYRLHRLAQP 175
DB 121 QMEELGMAPALOPTQGMPPAFASAFQRRAGGVLVASHLQSFLEVSRYRLHRLAQP 175

RESULT 10
ABG32030
ID ABG32030 standard; protein; 348 AA.
XX
AC ABG32030;
XX
XX 15-NOV-2002 (first entry)
DT
XX
DE Single chain G-CSF dimer polypeptide mutant, #2.
XX
XX Single-chain multimeric polypeptide; polyethylene glycol; PEG;
KW granulocyte colony stimulating factor; G-CSF; human;
KW haematopoietic disorder; radiation therapy; chemotherapy;
KW bone marrow transplantation; acquired immunodeficiency syndrome; AIDS;
KW immunodeficiency disease; leukopenia; acute myeloid leukaemia; half-life;
KW clearance; immunogenicity; bioavailability; single chain G-CSF dimer;
KW antihuman immunodeficiency virus; HIV; haemostatic; mutant; mutin.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Key 1.174
FT Region /note= "This region is copy 1 of the monomeric G-CSF
FT polypeptide encoded by either ABS52516 or ABS52519"
FT Misc-difference 16
FT /note= "Wild-type Lys substituted by Arg"
FT Misc-difference 34

```


FT Region /note= "wild-type Lys substituted by Arg"
 FT 175. .348
 FT /note= "This region is copy 2 of the monomeric G-CSF
 FT polypeptide encoded by ABS52517"
 FT Misc-difference 190
 FT /note= "wild-type Lys substituted by Arg"
 FT Misc-difference 208
 FT /note= "wild-type Lys substituted by Arg"
 XX WO200236626-A1.
 XX 10-MAY-2002.
 XX 01-NOV-2001; 2001WO-DK000724.
 XX 02-NOV-2000; 2000DK-00001647.
 XX (MAXY-) MAXYGEN APS.
 XX (MAXY-) MAXYGEN HOLDINGS LTD.
 XX Nissen TL, Jensen AD;
 XX PI
 XX WPI; 2002-618972/66.
 XX Single chain multimeric polypeptide conjugate for treating hematopoietic
 PT disorders, has two units of monomeric polypeptides linked via peptide
 PT bond/linker and polymer group bound to attachment group of polypeptide.
 PS Example 7; Page; 108pp; English.
 XX The invention discloses a single-chain multimeric polypeptide conjugate
 CC comprising at least two units of a monomeric polypeptide linked via a
 CC peptide bond or a peptide linker, where the monomeric polypeptide is
 CC biologically active in its monomeric form and has at least one polymer
 CC group covalently bound to an attachment group of the polypeptide e.g.
 CC polyethylene glycol (PEG). The polypeptide is preferably a single-chain
 CC multimeric granulocyte colony stimulating factor (G-CSF) polypeptide
 CC comprising at least two G-CSF polypeptide monomers, linked via a peptide
 CC bond or a peptide linker, where at least one of the monomers is a variant
 CC of wild-type human G-CSF comprising at least one amino acid residue
 CC modification. The monomeric and multimeric polypeptides are useful in
 CC therapy and for manufacture of a medicament for treatment of general
 CC haematopoietic disorders, including disorders arising from radiation
 CC therapy, chemotherapy or bone marrow transplantations, acquired
 CC immunodeficiency syndrome (AIDS) or other immunodeficiency diseases,
 CC leukaemia and acute myeloid leukaemia. The conjugate has one or more
 CC important properties as compared to the native polypeptide, including
 CC increased functional in vivo half-life, increased serum half-life,
 CC reduced clearance, reduced immunogenicity and/or increased
 CC bioavailability. Consequently, medical treatment with a conjugate offers
 CC advantages including longer duration between injections and fewer side
 CC effects. The sequence presented is the single chain G-CSF dimer
 CC polypeptide murätat, #2. Note: This sequence was not shown in the
 CC specification but was created by the indexer from information given in
 CC example 7
 XX Sequence 348 AA;
 SQ Query Match 99.1%; Score 893; DB 5; Length 348;
 Best Local Similarity 99.4%; Pred. No. 5e-89;
 Matches 173; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TPLGPASSLPQSFLRLCQLVRIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 61
 Db 1 TPLGPASSLPQSFLRLCQLVRIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
 QY 62 LSSCPSQALQAGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLVADPATTIQQ 121
 Db 61 LSSCPSQALQAGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLVADPATTIQQ 120
 QY 122 MEELGNAPALOPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 Db 121 MEELGNAPALOPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 11
 AAP71030
 ID AAP71030 standard; protein; 175 AA.
 XX
 AC AAP71030;
 XX
 DT 29-MAY-1991 (first entry)
 XX Sequence of human granulocyte colony stimulating factor (hGCSF) type II.
 DE Myelogenous leukaemia therapy; neutrophil.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "optional"
 XX
 PN EP231819-A.
 XX 12-AUG-1987.
 XX
 PF 21-JAN-1987; 87EP-00100809.
 XX
 PR 22-JAN-1986; 86JP-00010281.
 PR 21-JAN-1987; 87JP-00010038.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Tamura M, Hattori K;
 XX WPI; 1987-222837/32.
 DR
 XX Agent for treating myelogenous leukaemia - contains human granulocyte
 PT colony stimulating factor.
 XX
 PS Claim 3; Page 7; 7pp; English.
 XX hGCSF is the effective ingredient of an agent for the treatment of
 CC myelogenous leukaemia. The agent is used for increasing the no. of
 CC peripheral mature neutrophils in patients with myelogenous leukaemia and
 CC also prolonging life. Doses are 0.1-500, pref. 5-100 meg, 1-7 times/week.
 CC Type II hGCSF may be prep'd. as in EP 8601138.7
 XX
 SQ Sequence 175 AA;
 Query Match 99.0%; Score 892; DB 1; Length 175;
 Best Local Similarity 98.3%; Pred. No. 2.6e-89;
 Matches 172; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGPASSLPQSFLRLCQLVRIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
 Db 1 MTPLGPASSLPQSFLRLCQLVRIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
 QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLVADPATTIQQ 120
 Db 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLVADPATTIQQ 120
 QY 121 QMEELGNAPALOPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 Db 121 QMEELGNAPALOPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 RESULT 12
 AAP70732
 ID AAP70732 standard; protein; 175 AA.
 XX
 AC AAP70732;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-APR-1991 (first entry)

PI Edwards RM;
XX DR WPI; 1989-243775/34.
XX
XX Synthetic granulocyte colony stimulating factor gene - incorporating
PT restriction sites for facilitating cassette mutagenesis and expression.
XX
XX Disclosure; Fig 3a; 24pp; English.
XX
XX G-CSF stimulates proliferation of specific bone marrow precursor cells
CC and their differentiation into granulocytes. See also AAN90533. (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 175 AA;
SQ

Query Match 99.0%; Score 892; DB 1; Length 175;
Best Local Similarity 98.3%; Pred. No. 2.6e-89;
Matches 172; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
1 MTPLGPASSLPQSFLLRCLLEQVRKIQGDGAALQERLCATYRICHPEELVLLGHSLGIPWA 60
1 MTPLGPASSLPQSFLLRCLLEQVRKIQGDGAALQERLCATYRICHPEELVLLGHSLGIPWA 60
61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWO 120
61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWO 120
121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSYRVLRLHQAQP 175
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Job time : 64.5 secs

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Db 1 MTPLGPASSLPQSFLLRCLLEQVRKIQGDGAALQERLCATYRICHPEELVLLGHSLGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWO 120
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Db 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSYRVLRLHQAQP 175

RESULT 15
AAP91070
ID AAP91070 standard; protein; 175 AA.
XX
AC AAP91070;
XX
XX 25-MAR-2003 (revised)
DT 27-NOV-1989 (first entry)
XX
DE Human granulocyte colony stimulating factor.
XX
XX Human granulocyte colony stimulating factor; restriction sites;
KW bone marrow precursor cells.
XX
XX Homo sapiens.
XX
XX GB2213821-A.
PN
XX 23-AUG-1989.
PD
XX 23-DEC-1987; 87GB-00030055.
PF
XX 23-DEC-1987; 87GB-00030055.
PR
XX (BRBI-) BRIT BIO-TECHN LTD.
PA
XX Edwards RM;
PI
XX WPI; 1989-243775/34.
DR
XX Synthetic granulocyte colony stimulating factor gene - incorporating
PT restriction sites for facilitating cassette mutagenesis and expression.
XX
XX Disclosure; Fig 3a; 24pp; English.
PS
XX G-CSF stimulates proliferation of specific bone marrow precursor cells
CC and their differentiation into granulocytes. See also AAN90533. (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 175 AA;
SQ

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OM protein - protein search, using sw model

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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	901	100.0	175	1	US-08-010-099-2
2	901	100.0	175	1	US-08-167-721-1
3	901	100.0	175	1	US-08-428-732-6
4	901	100.0	175	1	US-08-448-716-2
5	901	100.0	175	2	US-08-321-510-2
6	901	100.0	175	2	US-08-879-760-2
7	901	100.0	175	3	US-09-304-186-2
8	901	100.0	175	4	US-09-230-733-1
9	901	100.0	175	4	US-09-479-313B-15
10	901	100.0	175	4	US-09-754-532-2
11	901	100.0	175	5	PCT-US95-01729-2
12	898	99.7	175	1	US-08-010-099-67
13	898	99.7	175	1	US-08-010-099-68
14	898	99.7	175	1	US-08-010-099-69
15	898	99.7	175	1	US-08-010-099-70
16	898	99.7	175	1	US-08-010-099-76
17	898	99.7	175	1	US-08-010-099-92
18	898	99.7	175	1	US-08-010-099-93
19	898	99.7	175	1	US-08-010-099-99
20	898	99.7	175	1	US-08-448-716-67
21	898	99.7	175	1	US-08-448-716-68
22	898	99.7	175	1	US-08-448-716-69
23	898	99.7	175	1	US-08-448-716-70
24	898	99.7	175	1	US-08-448-716-76
25	898	99.7	175	1	US-08-448-716-92
26	898	99.7	175	1	US-08-448-716-93
27	898	99.7	175	1	US-08-448-716-99

28	898	99.7	175	3	US-09-304-186-67	Sequence 67, Appl
29	898	99.7	175	3	US-09-304-186-68	Sequence 68, Appl
30	898	99.7	175	3	US-09-304-186-69	Sequence 69, Appl
31	898	99.7	175	3	US-09-304-186-70	Sequence 70, Appl
32	898	99.7	175	3	US-09-304-186-76	Sequence 76, Appl
33	898	99.7	175	3	US-09-304-186-92	Sequence 92, Appl
34	898	99.7	175	3	US-09-304-186-93	Sequence 93, Appl
35	898	99.7	175	3	US-09-304-186-99	Sequence 99, Appl
36	898	99.7	175	4	US-09-754-532-67	Sequence 67, Appl
37	898	99.7	175	4	US-09-754-532-68	Sequence 68, Appl
38	898	99.7	175	4	US-09-754-532-69	Sequence 69, Appl
39	898	99.7	175	4	US-09-754-532-70	Sequence 70, Appl
40	898	99.7	175	4	US-09-754-532-76	Sequence 76, Appl
41	898	99.7	175	4	US-09-754-532-92	Sequence 92, Appl
42	898	99.7	175	4	US-09-754-532-93	Sequence 93, Appl
43	898	99.7	175	4	US-09-754-532-99	Sequence 99, Appl
44	898	99.7	175	5	PCT-US95-01752-2	Sequence 2, Appli
45	898	99.7	177	2	US-08-797-689-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-010-099-2
; Sequence 2, Application US/08010099
; Patent No. 5581476
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen, Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER:
; APPLICATION NUMBER: US/08/010,099
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-010-099-2

Query Match 100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTPPLGPASSLPQSLKLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLHSLGIPWA	60
DB	1	MTPPLGPASSLPQSLKLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLHSLGIPWA	60
QY	61	PLSSCPQALQAGCISQLHSGFLYQGLQALEGISPELPTLDTLQLDVADFATTIQ	120
DB	61	PLSSCPQALQAGCISQLHSGFLYQGLQALEGISPELPTLDTLQLDVADFATTIQ	120

QY 121 QMEELGMAPALOPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYRVLRLHAQP 175
Db |||||
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RESULT 2

US-08-167-721-1
; Sequence 1, Application US/08167721
; Patent No. 5597562
; GENERAL INFORMATION:
; APPLICANT: No. 5597562ura, Hideaki
; APPLICANT: Maruyama, Kazutoshi
; TITLE OF INVENTION: Oral Dosage Form of Biologically Active
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,721
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/994,076
; FILING DATE:
; APPLICATION NUMBER: US/07/709,622
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 11009/30403
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-167-721-1

Query Match 100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
Db |||||
1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADPATTIWO 120
Db |||||
61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADPATTIWO 120
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Db |||||
121 QMEELGMAPALOPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYRVLRLHAQP 175

RESULT 3

US-08-428-732-6

; Sequence 6, Application US/08428732
; Patent No. 5606024
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Miller, Allan L.
; TITLE OF INVENTION: DNA Encoding Canine Granulocyte Colony
; TITLE OF INVENTION: Stimulating Factor (G-CSF)
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,732
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Crandall, Craig A.
; REFERENCE/DOCKET NUMBER: A-173-C2
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-428-732-6

Query Match 100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
Db |||||
1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADPATTIWO 120
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QY 121 QMEELGMAPALOPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYRVLRLHAQP 175
Db |||||
121 QMEELGMAPALOPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSRYRVLRLHAQP 175

RESULT 4

US-08-448-716-2
; Sequence 2, Application US/08448716
; Patent No. 5790421
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,716
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-448-716-2

Query Match      100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSGLGPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSGLGPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIQQ 120
QY 121 QMEELGMAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
DB 121 QMEELGMAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

;
; RESULT 5
; US-08-321-510-2
; Sequence 2, Application US/08321510
; Patent No. 5824784
; GENERAL INFORMATION:
; APPLICANT: Kinstler, Olaf B.
; APPLICANT: Gabriel, Nancy E.
; APPLICANT: Farrar, Christine E.
; APPLICANT: DePrince, Randolph B.
; TITLE OF INVENTION: N-Terminally Chemically Modified Protein
; TITLE OF INVENTION: Composition and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,510
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-286
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-321-510-2

Query Match      100.0%; Score 901; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSGLGPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSGLGPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIQQ 120
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DB 121 QMEELGMAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

;
; RESULT 6
; US-08-879-760-2
; Sequence 2, Application US/08879760
; Patent No. 5985265
; GENERAL INFORMATION:
; APPLICANT: Kinstler, Olaf B.
; APPLICANT: Gabriel, Nancy E.
; APPLICANT: Farrar, Christine E.
; APPLICANT: DePrince, Randolph B.
; TITLE OF INVENTION: N-Terminally Chemically Modified Protein
; TITLE OF INVENTION: Composition and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/879,760
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/321,510
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-286
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-879-760-2

Query Match      100.0%; Score 901; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSGLGPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSGLGPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIQQ 120
QY 121 QMEELGMAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
DB 121 QMEELGMAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

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QY 121 QMEELGMAPALQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSYRVLRLHAQP 175
Db 121 QMEELGMAPALQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSYRVLRLHAQP 175

RESULT 7

US-09-304-186-2
; Sequence 2, Application US/09304186
; Patent No. 6261550
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/304,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-304-186-2

Query Match 100.0%; Score 901; DB 3; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLLKCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
Db 1 MTPLGPASSLPQSFLLKCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
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Db 61 PLSSCPQALQAGLSQLHSGFLYQGLQALEGISPELGTDLTQLDVAADFATTIQQ 120
QY 121 QMEELGMAPALQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSYRVLRLHAQP 175
Db 121 QMEELGMAPALQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSYRVLRLHAQP 175

RESULT 8

US-09-230-733-1
; Sequence 1, Application US/09230733
; Patent No. 6583267
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, Motoo
; APPLICANT: Yamasaki, Toshiyuki
; APPLICANT: Kobayashi, Ken
; APPLICANT: Konishi, No. 6583267oru

; APPLICANT: Akinaga, Shiro
; APPLICANT: Matuyama, Kumiko
; TITLE OF INVENTION: CHEMICALLY MODIFIED POLYPEPTIDES
; FILE REFERENCE: 249-102
; CURRENT APPLICATION NUMBER: US/09/230,733
; CURRENT FILING DATE: 1999-02-03
; EARLIER APPLICATION NUMBER: PCT/JP98/02504
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: JP 9-149342
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: polypeptide
; OTHER INFORMATION: having hg-CSF activity
US-09-230-733-1

Query Match 100.0%; Score 901; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTPLGPASSLPQSFLLKCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQAGLSQLHSGFLYQGLQALEGISPELGTDLTQLDVAADFATTIQQ 120
Db 61 PLSSCPQALQAGLSQLHSGFLYQGLQALEGISPELGTDLTQLDVAADFATTIQQ 120
QY 121 QMEELGMAPALQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSYRVLRLHAQP 175
Db 121 QMEELGMAPALQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSYRVLRLHAQP 175

RESULT 9

US-09-479-313B-15
; Sequence 15, Application US/09479313B
; Patent No. 6627186
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEIN VARIANTS OF hg-CSF WITH GRANULOPOLYETIC
; FILE REFERENCE: A-67614-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/479,313B
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,131
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: US 60/118,831
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 15
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (2)..()

Query Match 100.0%; Score 901; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLLKCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
Db 1 MTPLGPASSLPQSFLLKCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60

QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQDVLADPATTIQQ 120
DB 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQDVLADPATTIQQ 120
QY 121 QMEELGMAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175
DB 121 QMEELGMAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175

RESULT 10

US-09-754-532-2
; Sequence 2, Application US/09754532
; Patent No. 6632426
; GENERAL INFORMATION:
; APPLICANT: Oeslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-01729-2

Query Match 100.0%; Score 901; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-754-532-2

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Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 QMEELGMAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175
DB 121 QMEELGMAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175

RESULT 11

PCT-US95-01729-2
; Sequence 2, Application PC/TUS9501729
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: N-Terminally Chemically Modified Protein

; TITLE OF INVENTION: Composition and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01729
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-286
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-01729-2

Query Match 100.0%; Score 901; DB 5; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCBPBELVLLGHSLGIPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCBPBELVLLGHSLGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQDVLADPATTIQQ 120
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QY 121 QMEELGMAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175
DB 121 QMEELGMAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175

RESULT 12

US-08-010-099-67
; Sequence 67, Application US/08010099
; Patent No. 5581476
; GENERAL INFORMATION:
; APPLICANT: Oeslund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen, Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/010,099
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol

NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: Amgen Center, 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/010,099
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-5725
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-010-099-70

Query Match 99.7%; Score 898; DB 1; Length 175;
Best Local Similarity 99.4%; Pred. No. 4.1e-92;
Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Job time : 22 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:14:34 ; Search time 297.5 Seconds
(without alignments)
211.245 Million cell updates/sec

Title: 10032108-2
Perfect score: 901
Sequence: 1 MTPGLPASSLPQSLFKCLE.....SHLQSFVSVYRLHRAQP 175

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Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	901	100.0	175	9	US-09-754-532-2 Sequence 2, Appli
2	901	100.0	175	9	US-09-230-733-1 Sequence 1, Appli
3	901	100.0	175	9	US-09-921-114-2 Sequence 2, Appli
4	901	100.0	175	11	US-09-817-725-2 Sequence 2, Appli
5	901	100.0	175	14	US-10-131-956-2 Sequence 2, Appli
6	901	100.0	175	14	US-10-264-846-2 Sequence 2, Appli
7	901	100.0	175	14	US-10-009-792A-21 Sequence 21, Appli
8	901	100.0	175	14	US-10-032-108-2 Sequence 2, Appli
9	901	100.0	175	14	US-10-345-639A-2 Sequence 2, Appli
10	901	100.0	175	14	US-10-365-418-1 Sequence 1, Appli
11	901	100.0	175	14	US-10-436-784-2 Sequence 2, Appli
12	901	100.0	175	14	US-10-168-956A-3 Sequence 3, Appli
13	901	100.0	175	15	US-10-632-695-15 Sequence 15, Appli

14	901	100.0	175	16	US-10-659-295-38 Sequence 38, Appli
15	901	100.0	175	16	US-10-750-797-2 Sequence 2, Appli
16	901	100.0	175	17	US-10-751-242-2 Sequence 2, Appli
17	898	99.7	175	9	US-09-754-532-67 Sequence 67, Appli
18	898	99.7	175	9	US-09-754-532-68 Sequence 68, Appli
19	898	99.7	175	9	US-09-754-532-69 Sequence 69, Appli
20	898	99.7	175	9	US-09-754-532-70 Sequence 70, Appli
21	898	99.7	175	9	US-09-754-532-76 Sequence 76, Appli
22	898	99.7	175	9	US-09-754-532-92 Sequence 92, Appli
23	898	99.7	175	9	US-09-754-532-93 Sequence 93, Appli
24	898	99.7	175	9	US-09-754-532-99 Sequence 99, Appli
25	898	99.7	175	9	US-09-818-430A-2 Sequence 2, Appli
26	898	99.7	175	14	US-10-032-108-67 Sequence 67, Appli
27	898	99.7	175	14	US-10-032-108-68 Sequence 68, Appli
28	898	99.7	175	14	US-10-032-108-69 Sequence 69, Appli
29	898	99.7	175	14	US-10-032-108-70 Sequence 70, Appli
30	898	99.7	175	14	US-10-032-108-76 Sequence 76, Appli
31	898	99.7	175	14	US-10-032-108-92 Sequence 92, Appli
32	898	99.7	175	14	US-10-032-108-93 Sequence 93, Appli
33	898	99.7	175	14	US-10-032-108-99 Sequence 99, Appli
34	898	99.7	177	9	US-09-984-186-14 Sequence 14, Appli
35	898	99.7	177	14	US-10-237-667-14 Sequence 14, Appli
36	898	99.7	177	14	US-10-237-708-14 Sequence 14, Appli
37	898	99.7	177	14	US-10-237-866-14 Sequence 14, Appli
38	898	99.7	177	14	US-10-237-871-14 Sequence 14, Appli
39	898	99.7	177	14	US-10-237-824-14 Sequence 14, Appli
40	898	99.7	177	15	US-10-702-536-14 Sequence 14, Appli
41	898	99.7	177	15	US-10-702-636-14 Sequence 14, Appli
42	898	99.7	759	15	US-10-609-346-8 Sequence 8, Appli
43	896	99.4	174	9	US-09-760-008A-1 Sequence 1, Appli
44	896	99.4	174	9	US-09-950-473-2 Sequence 2, Appli
45	896	99.4	174	9	US-09-921-114-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-754-532-2
; Sequence 2, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-2

Query Match      100.0%; Score 901; DB 9; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
DB 1 MTLPGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTPTLDTLQLDVADFATTIWO 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTPTLDTLQLDVADFATTIWO 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 2
US-09-230-733-1
; Sequence 1, Application US/09230733
; Patent No. US20020028912A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, Motoo
; APPLICANT: Suzawa, Toshiyuki
; APPLICANT: Kobayashi, Ken
; APPLICANT: Konishi, No. US20020028912A1oru
; APPLICANT: Akinaga, Shiro
; APPLICANT: Maruyama, Kumiko
; TITLE OF INVENTION: CHEMICALLY MODIFIED POLYPEPTIDES
; FILE REFERENCE: 249-102
; CURRENT APPLICATION NUMBER: US/09/230,733
; CURRENT FILING DATE: 1998-02-03
; EARLIER APPLICATION NUMBER: PCT/JP98/02504
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: JP 9-149342
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: polypeptide
; OTHER INFORMATION: having hG-CSF activity
US-09-230-733-1

Query Match      100.0%; Score 901; DB 9; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
DB 1 MTLPGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
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DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTPTLDTLQLDVADFATTIWO 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 3
US-09-921-114-2
; Sequence 2, Application US/09921114
; Patent No. US20020177688A1
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; GENERAL INFORMATION:
; APPLICANT: ISHIKAWA ET AL
; TITLE OF INVENTION: CHEMICALLY-MODIFIED G-CSF
; FILE REFERENCE: 11009/36193A
; CURRENT APPLICATION NUMBER: US/09/921,114
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 09/518,896
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 08/957,719
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: US 07/983,620
; PRIOR FILING DATE: 1992-11-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-921-114-2

Query Match      100.0%; Score 901; DB 9; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTPTLDTLQLDVADFATTIWO 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 4
US-09-817-725-2
; Sequence 2, Application US/09817725
; Publication No. US20040181035A1
; GENERAL INFORMATION:
; APPLICANT: Kinstler, Olaf B.
; Gabriel, Nancy E.
; Farrar, Christine B.
; DePrince, Randolph B.
; TITLE OF INVENTION: N-Terminally Chemically Modified Protein
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/817,725
; FILING DATE: 26-Mar-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/321,510
; FILING DATE: 1994-10-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-286
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-817-725-2

Query Match      100.0%; Score 901; DB 11; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
Db 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPGLPTLDTLQLDVADPATTIQQ 120
Db 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPGLPTLDTLQLDVADPATTIQQ 120
QY 121 QMEELGMAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
Db 121 QMEELGMAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 5
US-10-131-956-2
; Sequence 2, Application US/10131956
; Publication No. US20030053982A1
; GENERAL INFORMATION:
; APPLICANT: Kinntler, Olaf B.
; Gabriel, Nancy E.
; Farrar, Christine E.
; DePrince, Randolph B.
; TITLE OF INVENTION: N-Terminally Chemically Modified Protein
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 25-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/321,510
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-286
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-131-956-2

Query Match      100.0%; Score 901; DB 14; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPGLPTLDTLQLDVADPATTIQQ 120
Db 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPGLPTLDTLQLDVADPATTIQQ 120
QY 121 QMEELGMAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
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RESULT 6
US-10-264-846-2
; Sequence 2, Application US/10264846
; Publication No. US20030096400A1
; GENERAL INFORMATION:
; APPLICANT: Kinntler, Olaf B.
; Gabriel, Nancy E.
; Farrar, Christine E.
; DePrince, Randolph B.
; TITLE OF INVENTION: N-Terminally Chemically Modified Protein
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 04-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/264,846
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-286
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-264-846-2

Query Match      100.0%; Score 901; DB 14; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
Db 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPGLPTLDTLQLDVADPATTIQQ 120
Db 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPGLPTLDTLQLDVADPATTIQQ 120
QY 121 QMEELGMAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
Db 121 QMEELGMAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
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RESULT 7
 US-10-009-792A-21
 ; Sequence 21, Application US/10009792A
 ; Publication No. US20030153049A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEE, Sang-Yup
 ; APPLICANT: JEONG, Ki-Jun
 ; TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN
 ; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)
 ; FILE REFERENCE: HYLEE60 001APC
 ; CURRENT APPLICATION NUMBER: US/10/009,792A
 ; CURRENT FILING DATE: 2002-10-29
 ; PRIOR APPLICATION NUMBER: PCT/KR01/00549
 ; PRIOR FILING DATE: 2001-03-31
 ; PRIOR APPLICATION NUMBER: KR 10-2000-0017052
 ; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 21
 ; LENGTH: 175
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-009-792A-21

Query Match 100.0%; Score 901; DB 14; Length 175;
 Best Local Similarity 100.0%; Pred. No. 9.3e-84;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
 Db 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
 QY 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALEGISELPGTDLTLDVADFAATTIQ 120
 Db 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALEGISELPGTDLTLDVADFAATTIQ 120
 QY 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
 Db 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

RESULT 8
 US-10-032-108-2
 ; Sequence 2, Application US/10032108
 ; Publication No. US20030171559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Oselund, Timothy
 ; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
 ; FILE REFERENCE: 01017/38834F
 ; CURRENT APPLICATION NUMBER: US/10/032,108
 ; CURRENT FILING DATE: 2003-01-31
 ; PRIOR APPLICATION NUMBER: US 09/754,532
 ; PRIOR FILING DATE: 2001-01-03
 ; PRIOR APPLICATION NUMBER: US 09/304,186
 ; PRIOR FILING DATE: 1999-05-03
 ; PRIOR APPLICATION NUMBER: US 09/027,508
 ; PRIOR FILING DATE: 1998-02-20
 ; PRIOR APPLICATION NUMBER: US 08/956,812
 ; PRIOR FILING DATE: 1987-10-23
 ; PRIOR APPLICATION NUMBER: US 08/448,716
 ; PRIOR FILING DATE: 1995-05-24
 ; PRIOR APPLICATION NUMBER: US 08/010,099
 ; PRIOR FILING DATE: 1993-01-28
 ; NUMBER OF SEQ ID NOS: 110
 ; SOFTWARE: Patent-In ver. 3.1
 ; SEQ ID NO 2
 ; LENGTH: 175
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-032-108-2

Query Match 100.0%; Score 901; DB 14; Length 175;

Best Local Similarity 100.0%; Pred. No. 9.3e-84;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
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 QY 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALEGISELPGTDLTLDVADFAATTIQ 120
 Db 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALEGISELPGTDLTLDVADFAATTIQ 120
 QY 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
 Db 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

RESULT 9
 US-10-345-639A-2
 ; Sequence 2, Application US/10345639A
 ; Publication No. US20030185795A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Habberfield, Alan D.
 ; TITLE OF INVENTION: Oral Delivery of Chemically Modified Proteins
 ; FILE REFERENCE: A-285G
 ; CURRENT APPLICATION NUMBER: US/10/345,639A
 ; CURRENT FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 09/818,430
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 08/910,814
 ; PRIOR FILING DATE: 1997-08-13
 ; PRIOR APPLICATION NUMBER: 08/753,901
 ; PRIOR FILING DATE: 1996-12-03
 ; PRIOR APPLICATION NUMBER: 08/379,121
 ; PRIOR FILING DATE: 1995-02-01
 ; PRIOR APPLICATION NUMBER: 08/361,016
 ; PRIOR FILING DATE: 1994-12-21
 ; PRIOR APPLICATION NUMBER: 08/194,187
 ; PRIOR FILING DATE: 1994-02-08
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 175
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-345-639A-2

Query Match 100.0%; Score 901; DB 14; Length 175;
 Best Local Similarity 100.0%; Pred. No. 9.3e-84;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
 Db 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
 QY 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALEGISELPGTDLTLDVADFAATTIQ 120
 Db 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALEGISELPGTDLTLDVADFAATTIQ 120
 QY 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
 Db 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

RESULT 10
 US-10-365-418-1
 ; Sequence 1, Application US/10365418
 ; Publication No. US20030195339A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yamasaki, Motoo
 ; APPLICANT: Suzawa, Toshiyuki
 ; APPLICANT: Kobayashi, Ken
 ; APPLICANT: Konishi, No. US20030195339A1or
 ; APPLICANT: Akinaga, Shiro

Query Match 100.0%; Score 901; DB 15; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPOSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
DB 1 MTPLGPASSLPOSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60

QY 61 PLSSCPSQALQALAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTTIWQ 120
DB 61 PLSSCPSQALQALAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTTIWQ 120

QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 14
US-10-659-295-38
; Sequence 38, Application US/10659295
; Publication No. US20040141946A1
; GENERAL INFORMATION:
; APPLICANT: SCHNEIDER, ARMIN
; APPLICANT: SCHAEBITZ, WOLF-RUEDIGER
; APPLICANT: KOLLMAR, RAINER
; APPLICANT: SCHWAB, STEFAN
; TITLE OF INVENTION: METHODS OF TREATING NEUROLOGICAL CONDITIONS WITH HEMATOPOIETIC OR
; FILE REFERENCE: 229530US
; CURRENT APPLICATION NUMBER: US/10/659,295
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/10/331,755
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-295-38

Query Match 100.0%; Score 901; DB 16; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPOSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
DB 1 MTPLGPASSLPOSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60

QY 61 PLSSCPSQALQALAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTTIWQ 120
DB 61 PLSSCPSQALQALAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTTIWQ 120

QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 15
US-10-750-797-2
; Sequence 2, Application US/10750797
; Publication No. US20040158041A1
; GENERAL INFORMATION:
; APPLICANT: ISHIKAWA ET AL
; TITLE OF INVENTION: CHEMICALLY-MODIFIED G-CSF
; FILE REFERENCE: 11009/36193A
; CURRENT APPLICATION NUMBER: US/10/750,797
; CURRENT FILING DATE: 2004-01-02
; PRIOR APPLICATION NUMBER: US 09/518,896
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 08/957,719
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: US 07/983,620

; PRIOR FILING DATE: 1992-11-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-750-797-2

Query Match 100.0%; Score 901; DB 16; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPOSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
DB 1 MTPLGPASSLPOSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60

QY 61 PLSSCPSQALQALAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTTIWQ 120
DB 61 PLSSCPSQALQALAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTTIWQ 120

QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

Search completed: December 27, 2004, 13:34:27
Job time : 299.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:11:24 ; Search time 63.5 Seconds
(without alignments)
988.624 Million cell updates/sec

Title: 10032108-2
Perfect score: 901
Sequence: 1 MTPPLGPASSLPQSFLKCLE.....SHLQSFLEVSRYVLRHLAQP 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	901	100.0	175	1 AAP71030	Aap71030 Sequence
2	901	100.0	175	1 AAP70732	Aap70732 Sequence
3	901	100.0	175	1 AAP90107	Aap90107 Human gra
4	901	100.0	175	1 AAP90170	Aap90170 Human gra
5	901	100.0	175	1 AAP91070	Aap91070 Human gra
6	901	100.0	175	2 AA08486	Platelet
7	901	100.0	175	2 AA07533	Recombina
8	901	100.0	175	2 AA04394	PEGylated
9	901	100.0	175	2 AA084297	Human gra
10	901	100.0	175	3 AA078936	Granulocy
11	901	100.0	175	3 AA014851	Human gra
12	901	100.0	175	3 AA097017	Mature gr
13	901	100.0	175	3 AA023758	Human gra
14	901	100.0	175	4 AA067563	Amino aci
15	901	100.0	175	4 AA067502	Human hg-
16	901	100.0	175	4 AA012154	Human G-C
17	901	100.0	175	4 AA02109	Recombina
18	901	100.0	175	4 AA051536	Recombina
19	901	100.0	175	5 AA019311	Branch
20	901	100.0	175	6 AA097386	Recombina
21	901	100.0	175	8 AA043080	Recombina
22	901	100.0	317	2 AA023600	Recombina
23	898	99.7	175	2 AA056562	G-CSF ana
24	898	99.7	175	2 AA056585	G-CSF ana
25	898	99.7	175	2 AA056555	G-CSF ana

ALIGNMENTS

RESULT 1				
AAP71030				
ID	AAP71030	standard; protein; 175 AA.		
XX				
AC	AAP71030;			
XX				
DT	29-MAY-1991	(first entry)		
XX				
DE	Sequence of human granulocyte colony stimulating factor (hGCSF) type II.			
XX				
KW	Myelogenous leukaemia therapy; neutrophil.			
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	Misc-difference 1			
FT	/note= "optional"			
XX				
PN	EP231819-A.			
XX				
PD	12-AUG-1987.			
XX				
PF	21-JAN-1987;	87EP-00100809.		
XX				
PR	22-JAN-1986;	86JP-00010281.		
XX	21-JAN-1987;	87JP-00010038.		
PA	(CHUS) CHUGAI SEIYAKU KK.			
XX				
PI	Tamura M, Hattori K;			
XX	WPI; 1987-222837/32.			
DR	Agent for treating myelogenous leukaemia - contains human granulocyte colony stimulating factor.			
PT	Claim 3; Page 7; 7pp; English.			
XX				
PS	hGCSF is the effective ingredient of an agent for the treatment of myelogenous leukaemia. The agent is used for increasing the no. of peripheral mature neutrophils in patients with myelogenous leukaemia and also prolonging life. Doses are 0.1-500, pref. 5-100 meg, 1-7 times/week.			
XX	Type II hGCSF may be prepd. as in EP 8601138.7			
CC	Sequence 175 AA;			
XX				
Query Match	100.0%; Score 901; DB 1; Length 175;			
Best Local Similarity	100.0%; Pred. No. 1.9e-90;			

Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
 DB 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
 QY 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTPTLDTLQLDVADFAATTIQQ 120
 DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTPTLDTLQLDVADFAATTIQQ 120
 QY 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175
 DB 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175

RESULT 2
 AAP70732
 ID AAP70732 standard; protein; 175 AA.
 XX AAP70732;
 AC AAP70732;
 DT 25-MAR-2003 (revised)
 DT 26-APR-1991 (first entry)
 XX Sequence encoded by human granulocyte colony stimulating factor (hpg-CSF)
 DE CDNA with an amino terminal methionine.
 XX Haematopoietic disorders; therapy; aplastic anaemia;
 KW bone marrow transplant; burn wounds; leukaemia.
 XX Homo sapiens.
 XX WO8701132-A.
 XX 26-FEB-1987.
 XX 22-AUG-1986; 86WO-US001708.
 XX 23-AUG-1985; 85US-00768954.
 PR 23-AUG-1985; 85US-00768959.
 PR 03-MAR-1986; 86US-00835548.
 XX (KIRI) KIRIN AMGEN INC.
 PA (KIRI) KIRIN AMGEN INC.
 PA (AMGE-) AMGEN.
 XX Souza LM;
 PI WPI; 1987-064855/09.
 DR N-PSDB; AAN71091.
 XX Poly:peptide with granulocyte colony stimulating factor activity - obt'd.
 PT by recombinant DNA procedures for treating haematopoietic disorders.
 XX Example; pp42-43; 79pp; English.
 XX The examples describe procedures for the designing of probes for hpg- CSF
 CC cDNA and genomic clones, both of which are claimed. Specifically claimed
 CC are DNA sequences coding for (Ala 1)hpg-CSF; (Ser 36,42,64 and 74)hpg-CSF
 CC and the corresp. Met-1 cpds. The novelty is that hpg- CSF is the prod. of
 CC procarcynotic or eucarcynotic expression of an exogenous DNA sequence. The
 CC construction of hpg-CSF vectors is also described in the examples.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX Sequence 175 AA;
 SQ Query Match 100.0%; Score 901; DB 1; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.9e-90;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
 DB 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
 QY 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTPTLDTLQLDVADFAATTIQQ 120
 DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTPTLDTLQLDVADFAATTIQQ 120
 QY 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175
 DB 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175

RESULT 3
 AAP90107
 ID AAP90107 standard; protein; 175 AA.
 XX AAP90107;
 AC AAP90107;
 DT 25-MAR-2003 (revised)
 DT 27-NOV-1989 (first entry)
 XX Human granulocyte colony stimulating factor.
 DE Human granulocyte colony stimulating factor; restriction sites;
 KW bone marrow precursor cells.
 XX Homo sapiens.
 XX GB2213821-A.
 XX 23-AUG-1989.
 PD 23-DEC-1987; 87GB-00030055.
 PF 23-DEC-1987; 87GB-00030055.
 PR 23-DEC-1987; 87GB-00030055.
 XX (BRBI-) BRIT BIO-TECHN LTD.
 PA Edwards RM;
 PI WPI; 1989-243775/34.
 DR Synthetic granulocyte colony stimulating factor gene - incorporating
 PT restriction sites for facilitating cassette mutagenesis and expression.
 XX Disclosure; Fig 3a; 24pp; English.
 XX G-CSF stimulates proliferation of specific bone marrow precursor cells
 CC and their differentiation into granulocytes. See also AAN90533. (Updated
 CC on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
 CC PA field.)
 XX Sequence 175 AA;
 SQ Query Match 100.0%; Score 901; DB 1; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.9e-90;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
 DB 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
 QY 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTPTLDTLQLDVADFAATTIQQ 120
 DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGTPTLDTLQLDVADFAATTIQQ 120
 QY 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175
 DB 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175

RESULT 4
 AAP90170
 ID AAP90170 standard; protein; 175 AA.

```

XX AC AAP901070;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 27-NOV-1989 (first entry)
XX DE Human granulocyte colony stimulating factor.
XX XX
XX KW Human granulocyte colony stimulating factor; restriction sites;
XX KW bone marrow precursor cells.
XX OS Homo sapiens.
XX XX
XX PN GB2213821-A.
XX XX
XX PD 23-AUG-1989.
XX XX
XX PF 23-DEC-1987; 87GB-00030055.
XX XX
XX PR 23-DEC-1987; 87GB-00030055.
XX XX
XX PA (BRBI-) BRIT BIO-TECHN LTD.
XX XX
XX PI Edwards RM;
XX XX
XX DR WPI; 1989-243775/34.
XX XX
XX PT Synthetic granulocyte colony stimulating factor gene - incorporating
XX PT restriction sites for facilitating cassette mutagenesis and expression.
XX XX
XX PS Disclosure; Fig 3a; 24pp; English.
XX CC G-CSF stimulates proliferation of specific bone marrow precursor cells
XX CC and their differentiation into granulocytes. See also AAN90533. (Updated
XX CC on 25-MAR-2003 to correct PA field.)
XX XX
XX SQ Sequence 175 AA;

Query Match 100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQLAGLSQLHSGFLYQGLLQALEGISPELGTDLTQLDQVADFATTIQ 120
DB 61 PLSSCPSQLAGLSQLHSGFLYQGLLQALEGISPELGTDLTQLDQVADFATTIQ 120
QY 121 QMEELGMALOPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMALOPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 5
AAP91070
ID AAP91070 standard; protein; 175 AA.
XX AC AAP91070;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 27-NOV-1989 (first entry)
XX DE Human granulocyte colony stimulating factor.
XX XX
XX KW Human granulocyte colony stimulating factor; restriction sites;
XX KW bone marrow precursor cells.
XX OS Homo sapiens.
XX XX
XX PN GB2213821-A.
XX XX
XX PD 23-AUG-1989.
XX XX
XX PF 23-DEC-1987; 87GB-00030055.
XX XX
XX PR 23-DEC-1987; 87GB-00030055.
XX XX
XX PA (BRBI-) BRIT BIO-TECHN LTD.
XX XX
XX PI Edwards RM;
XX XX
XX DR WPI; 1989-243775/34.
XX XX
XX PT Synthetic granulocyte colony stimulating factor gene - incorporating
XX PT restriction sites for facilitating cassette mutagenesis and expression.
XX XX
XX PS Disclosure; Fig 3a; 24pp; English.
XX CC G-CSF stimulates proliferation of specific bone marrow precursor cells
XX CC and their differentiation into granulocytes. See also AAN90533. (Updated
XX CC on 25-MAR-2003 to correct PA field.)
XX XX
XX SQ Sequence 175 AA;

Query Match 100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQLAGLSQLHSGFLYQGLLQALEGISPELGTDLTQLDQVADFATTIQ 120
DB 61 PLSSCPSQLAGLSQLHSGFLYQGLLQALEGISPELGTDLTQLDQVADFATTIQ 120
QY 121 QMEELGMALOPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMALOPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 6
AAW08486
ID AAW08486 standard; protein; 175 AA.
XX AC AAW08486;
XX XX
XX DT 03-MAR-1997 (first entry)
XX XX
XX DE Platelet growth accelerator.
XX KW Platelet growth accelerator; granulocyte colony stimulating factor;
XX KW G-CSF; human; therapy; thrombocytopaenia.
XX OS Homo sapiens.
XX XX
XX PN WO9523165-A1.
XX XX
XX PD 31-AUG-1995.
XX XX
XX PF 23-FEB-1995; 95WO-JP000266.
XX XX
XX PR 23-FEB-1994; 94JP-00025735.
XX XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX XX
XX PI Yamaaki M, Okabe M, Suzawa T, Kobayashi K, Maruyama K;
XX DR WPI; 1995-320309/41.
XX XX
XX PT platelet growth accelerator contg. modified hG-CSF - for treatment of
XX PT thrombocytopaenia.
XX XX
XX PS Claim 2; Page 35-36; 46pp; Japanese.

```

XX This sequence represents a platelet growth accelerator of the invention.
CC This sequence contains a human granulocyte colony stimulating factor (G-CSF) peptide. The G-CSF peptide contains at least one amino carboxy, mercapto or guanidino group chemically modified. This platelet growth accelerator can be used in the treatment of thrombocytopaenia
XX Sequence 175 AA;

Query Match 100.0%; Score 901; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTPLGPASSLPQSFLKCLQEVKRIQGDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLKCLQEVKRIQGDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
OY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTDLTLDVADPATTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTDLTLDVADPATTIWQ 120
OY 121 QMEELGWAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGWAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 7
AAW07533
ID AAW07533 standard; protein; 175 AA.
AC AAW07533;
XX
DT 07-MAR-1997 (first entry)
XX
DE Recombinant human G-CSF, for use in novel powder.
XX
KW Powder; granulocyte colony stimulating factor; G-CSF; recombinant; human;
KW saccharide; mannitol; lactose; administration; drug;
KW myelopoietic function; improvement; nasal membrane.
XX
OS Homo sapiens.
XX
XX JP08198772-A.
XX
XX 06-AUG-1996.
XX
XX 01-MAR-1995; 95JP-00041734.
XX
XX 25-NOV-1994; 94JP-00291765.
XX
XX (KIRI) KIRIN BREWERY KK.
XX
XX WPI; 1996-408328/41.
XX
XX A powdery compsn. contg. G-CSF and a saccharide - for nasal
PT administration, is useful for improving myelopoietic functions.
XX
XX Example 1; Page 6; 8pp; Japanese.
XX
XX The novel powder of the invention contains granulocyte colony stimulating
CC factor (G-CSF), e.g. the present sequence, and a saccharide, pref.
CC mannitol or lactose. It can be used for the admin. of G-CSF, an important
CC drug for the improving myelopoietic function, via the nasal membranes, as
CC the saccharide enables a higher drug absorbability to be attained without
CC damaging the nasal membranes
XX
XX Sequence 175 AA;

Query Match 100.0%; Score 901; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTPLGPASSLPQSFLKCLQEVKRIQGDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60

DB 1 MTPLGPASSLPQSFLKCLQEVKRIQGDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
OY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTDLTLDVADPATTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTDLTLDVADPATTIWQ 120
OY 121 QMEELGWAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGWAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 8
AAR94394
ID AAR94394 standard; protein; 175 AA.
XX
AC AAR94394;
XX
DT 28-NOV-1996 (first entry)
XX
DE PEGylated recombinant human granulocyte colony stimulating factor.
XX
KW Recombinantly produced; human granulocyte colony stimulating factor;
KW rh-G-CSF; polyethylene glycol; PEG; stable; PEGylated G-CSF;
KW haematopoietic disorder; interferon; cell proliferative disorder;
KW viral infection; autoimmune disorder; multiple sclerosis.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "PEGylated-Met"
FT
XX
XX WO9611953-A1.
XX
XX 25-APR-1996.
XX
XX 08-FEB-1995; 95WO-US001729.
XX
XX 12-OCT-1994; 94US-00321510.
XX
XX (AMGE-) AMGEN INC.
XX
XX Kinstler OB, Gabriel NE, Farrar CE, Deprince RB;
XX
XX WPI; 1996-221948/22.
XX
XX N-PSDB; AAT14329.
XX
XX N-terminally chemically modified proteins - partic. G-CSF or consensus
PT interferon modified with polymers, esp. polyethylene glycol.
XX
XX Claim 8; Page 47-48; 76pp; English.
XX
XX This sequence encodes recombinantly produced human granulocyte colony
CC stimulating factor (rh-G-CSF). The G-CSF protein may be N-terminally
CC modified by polyethylene glycol in the preparation of the invention. The
CC PEGylation of the G-CSF makes the protein more stable and therefore more
CC suitable for therapeutic uses. The PEGylated G-CSF can be used for
CC treating haematopoietic disorders. A similarly modified interferon can be
CC used for treating cell proliferative disorders, viral infections or
CC autoimmune disorders, such as multiple sclerosis
XX
XX Sequence 175 AA;

Query Match 100.0%; Score 901; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTPLGPASSLPQSFLKCLQEVKRIQGDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLKCLQEVKRIQGDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
OY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTDLTLDVADPATTIWQ 120

Db 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLDQVADPATTIQ 120
QY 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
Db 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
RESULT 9
AAW84297
ID AAW84297 standard; protein; 175 AA.
XX AAW84297;
DT 19-MAR-1999 (first entry)
DE Human granulocyte colony stimulating factor (hGCSF).
XX Human granulocyte colony stimulating factor; hGCSF;
KW chemical modification; hydroxyl group; polyethyleneglycol;
KW platelet reduction; granulocyte reduction.
XX Homo sapiens.
OS Homo sapiens.
XX WO9855500-A1.
PN 10-DEC-1998.
XX 05-JUN-1998; 98WO-JP002504.
PF 06-JUN-1997; 97JP-00149342.
PR (KYOW) KYOWA HAKKO KOGYO KK.
XX Yamaeaki M, Suzawa T, Kobayashi K, Konishi N, Akinaga S;
PI Maruyama K;
XX WPI; 1999-059899/05.
DR New Chemically modified polypeptides especially granulocyte-colony
PT stimulating factor - has hydroxy group modified with polyethylene glycol.
XX Claim 4; Page 34-35; 45pp; Japanese.
XX The present sequence represents human granulocyte colony stimulating
CC factor (hGCSF). The protein was modified to exemplify the invention. The
CC specification describes a method for chemically modifying polypeptides so
CC that at least one of their hydroxyl groups is modified with
CC polyethyleneglycol. The chemically modified proteins are especially
CC useful for preventing a reduction in platelets or granulocytes, and are
CC more active and longer lasting than the unmodified peptides
XX Sequence 175 AA;
QY Query Match 100.0%; Score 901; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGSHLGPWA 60
Db 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGSHLGPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLDQVADPATTIQ 120
Db 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLDQVADPATTIQ 120
QY 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
Db 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
RESULT 10
AAW78936
ID AAW78936 standard; protein; 175 AA.
XX AAW78936;
DT 05-JUN-2000 (first entry)
DE Granulocyte colony-stimulation factor (G-CSF) peptide sequence #1.
XX Granulocyte colony-stimulation factor; G-CSF; powder preparation;
KW polymeric drug administration; mucus membrane.
XX Homo sapiens.
OS Homo sapiens.
XX WO200002574-A1.
PN 20-JAN-2000.
XX 01-JUL-1999; 99WO-JP003563.
PF 08-JUL-1998; 98JP-00192722.
PR 25-MAR-1999; 99JP-00081549.
XX (KIRI) KIRIN AMGEN INC.
XX Nomura H, Ueki Y;
PI WPI; 2000-182173/16.
DR Powder preparation for mucosal administration of polymeric drug, e.g.
PT peptide, protein, antibody, vaccine or antigen.
XX Disclosure; Page 38-39; 45pp; Japanese.
XX This sequence represents a human granulocyte colony-stimulating factor (G
CC -CSF) polypeptide. G-CSF is used in a powder preparation which is
CC administered via the mucus membrane. The preparation comprises a
CC polymeric medicine and a cationic polymer. The preparation is used for
CC the mucosal administration of polymeric pharmaceuticals and has good
CC absorption through the mucous membrane and improved bioavailability
XX Sequence 175 AA;
QY Query Match 100.0%; Score 901; DB 3; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGSHLGPWA 60
Db 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGSHLGPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLDQVADPATTIQ 120
Db 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLDQVADPATTIQ 120
QY 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
Db 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
RESULT 11
AAW14851
ID AAW14851 standard; protein; 175 AA.
XX AAW14851;
XX 19-DEC-2000 (first entry)
DE Human granulocyte colony stimulating factor #2.
XX Human granulocyte colony stimulating factor; G-CSF; neutropaenia;
KW bone marrow suppression; infection.
XX Homo sapiens.
OS Homo sapiens.

XX WO200040728-A1.
 XX 13-JUL-2000.
 XX 06-JAN-2000; 2000WO-US000300.
 XX 06-JAN-1999; 99US-0115131P.
 XX 05-FEB-1999; 99US-0118831P.
 XX (XENC-) XENCOR INC.
 XX Dahiyat B, Luo P;
 XX WPI; 2000-465988/40.
 XX
 XX A non-naturally occurring granulopoietic activity protein (GPA) for
 XX treating granulocyte colony stimulating factor (G-CSF)-responsive disease
 XX comprises an amino acid sequence less than 95% identical to hG-CSF.
 XX
 XX Disclosure; Fig 3; 63pp; English.
 XX
 XX The present sequence is the protein sequence for the human granulocyte
 XX colony stimulating factor (G-CSF). This protein is involved in the
 XX proliferation and differentiation of granulocytes in the blood. The
 XX sequence was used to create the proteins of the invention, which are
 XX designated granulopoietic activity (GPA) proteins. These can be used
 XX instead of G-CSF, which has a short half-life in the blood and is
 XX unstable in storage, in treatments for neutropenia associated with
 XX cancer therapies, radiation accidents, bone marrow transplantation, bone
 XX marrow suppression conditions such as AIDS, myelodysplastic syndromes
 XX characterised by granulocyte functional abnormalities, and severe
 XX infections. They can also be used to enhance peripheral blood progenitor
 XX cell collection
 XX
 XX Sequence 175 AA;

Query Match 100.0%; Score 901; DB 3; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.9e-90;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGPAASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHEPELVLLGHSIGIPWA 60
 DB 1 MTPLGPAASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHEPELVLLGHSIGIPWA 60
 QY 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLQDVADFTATTIQ 120
 DB 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLQDVADFTATTIQ 120
 QY 121 QMEELGNAPALQPTQGMAMPASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 DB 121 QMEELGNAPALQPTQGMAMPASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 12
 AAY97017
 ID AAY97017 standard; protein; 175 AA.

XX AAY97017;
 XX AC
 XX 31-OCT-2000 (first entry)
 XX DE Mature granulocyte colony stimulating factor.

XX G-CSF; granulocyte colony stimulating factor; sustained-release;
 XX biocompatible polyol/oil suspension; anti-inflammatory.

XX Homo sapiens.
 XX WO200038652-A1.
 XX 06-JUL-2000.

PF 20-DEC-1999; 99WO-US030527.
 XX
 XX 23-DEC-1998; 98US-00221181.
 PR 23-NOV-1999; 99US-00448205.
 XX
 XX (AMGE-) AMGEN INC.
 XX Goldenberg MS, Shan D, Beekman AC;
 XX WPI; 2000-452289/39.
 XX
 XX Pharmaceutical composition for the sustained-release of a biologically
 XX active agent (BAA), such as granulocyte-colony stimulating factor,
 XX comprises incorporating the BAA into a biocompatible polyol/oil
 XX suspension.
 XX
 XX Claim 7; Page; 38pp; English.
 XX
 XX A pharmaceutical composition comprising a biologically active agent (BAA)
 XX incorporated into a biocompatible polyol/oil suspension which contains a
 XX thickener is new. The compositions are used for the sustained-release of
 XX a BAA such as an interferon consensus, EPO, granulocyte-colony
 XX stimulating factor, stem cell factor, leptin, tumor necrosis factor-
 XX binding protein, interleukin-1 receptor antagonist, brain derived
 XX neurotrophic factor, glial derived neurotrophic factor, neutrophilic factor
 XX 3, osteoprotegerin, granulocyte macrophage colony stimulating factor,
 XX megakaryocyte derived growth factor, keratinocyte growth factor,
 XX thrombopoietin, or novel erythropoiesis stimulating protein (claimed).
 XX The release of a medicament can be controlled to provide longer periods
 XX of consistent release that previous methods of treatment do not achieve,
 XX such as repeated injections. Blood levels of the active ingredient can be
 XX controlled, providing an enhanced prophylactic, therapeutic, or
 XX diagnostic effect as well as greater safety, patient convenience and
 XX patient compliance. The compositions can lead to dose sparing and a lower
 XX cost of protein production. Bioavailability and protein protection,
 XX stability and potency are increased. Note: This sequence is not given in
 XX the specification, it was created using the mature protein starting at
 XX threonine (shown in AAY97017) is given on page 11
 XX
 XX Sequence 175 AA;

Query Match 100.0%; Score 901; DB 3; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.9e-90;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPAASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHEPELVLLGHSIGIPWA 60
 DB 1 MTPLGPAASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHEPELVLLGHSIGIPWA 60
 QY 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLQDVADFTATTIQ 120
 DB 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLQDVADFTATTIQ 120
 QY 121 QMEELGNAPALQPTQGMAMPASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 DB 121 QMEELGNAPALQPTQGMAMPASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 13
 AAB23758
 ID AAB23758 standard; protein; 175 AA.

XX AAB23758;
 XX AC
 XX 10-JAN-2001 (first entry)
 XX DE Human granulocyte colony stimulating factor protein SEQ ID NO:1.
 XX
 XX Granulocyte colony stimulating factor; G-CSF; CRH-G-CSF-R;
 XX protein co-ordinate data; immunostimulant; identification; mutant;
 XX agonist; antagonist; computer modelling; neutropenia;
 XX three dimensional structure; chemotherapy; radiotherapy; cancer.

XX New three-dimensional structural coordinate of a protein complex of
PT leptin and its receptor binding domain, for identifying and designing
PT leptin mutants with superior biological activity, or agonists and
PT antagonists.
XX
PS Example 1; Page 673-674; 683pp; Japanese.
XX
CC The specification describes a three-dimensional (3D) structural
CC coordinate of a complex formed from leptin and a binding domain of its
CC receptor (CRH-leptin receptor). The 3D structural coordinate is
CC applicable in identifying, searching, evaluating or designing leptin
CC mutants with superior biological activity or its agonists and antagonists
CC after mutation or modification, particularly for providing effect on
CC arcuate nuclei, and in inhibiting intake or reducing weight loss. The
CC present sequence represents a human protein, designated G-CSF. The
CC protein is used in the course of the invention
XX
SQ Sequence 175 AA;

Query Match 100.0%; Score 901; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTPIGPASSLPQSFLKCLQVVRKIQGDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
Db 1 MTPIGPASSLPQSFLKCLQVVRKIQGDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60

Qy 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQ 120
Db 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQ 120

Qy 121 QMEELGNAPALQPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
Db 121 QMEELGNAPALQPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

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